

## STIC Search Report Biotech-Chem Library

## STO Database termination

TO: Cynthia Wilder

Location: REM/2A35/2C18

Wednesday, April 20, 2005

Art Unit: 1637

Case Serial Number: 09/529397

From: David Schreiber

**Location: Biotech-Chem Library** 

Remsen E01A61

Phone: 571-272-2526

David.Schreiber@uspto.gov

	Search Notes	0	
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5.1.6	Compugen Ltd
enCore version 5.1.6	- 2005
GenCore	(c) 1993
	Copyright

- nucleic search, using sw model OM nucleic

Run on:

April 19, 2005, 13:28:09; Search time 427 Seconds (without alignments) 1386.356 Million cell updates/sec

US-09-529-397C-25 Perfect score:

1 gggaguggaggaauucaucg......uagcgacagcaagcuucugc 100 Sequence:

Gapop 10.0 , Gapext 1.0 IDENTITY NUC Scoring table:

4390206 segs, 2959870667 residues

Searched:

8780412 Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries seq length: 0 seq length: 200000000 Minimum DB Maximum DB

16Dec04:\* Genesed

geneseqn2003cs:\* geneseqn2003ds:\* geneseqn2003as:\* geneseqn2001as:\* geneseqn2002as:\* geneseqn2002bs:\* geneseqn2003bs:\* geneseqn2001bs:\* geneseqn1990s:\* geneseqn2000s:\* geneseqn1980s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

geneseqn2004as:\* geneseqn2004bs:\*

SUMMARIES

Description Ω В Length Query Result No.

Adj10063 Synthetic Adj10064 Synthetic Adj10065 Synthetic Aaz9050 RNA aptam Adj10053 RNA aptam Aaz99051 RNA aptam Adq97596 Mouse can Aaz57942 Poplar fl Synthetic DNA encod RNA aptam Human ORF Human ORF Aaz99076 Ras targe Aac75113 Human ORF Propionib Nucleotid Aaz99048 RNA aptam Propionib Poplar Poplar Adj10066 Aas59583 | Acf64512 | Ada29321 | Aaf85391 N Abk88484 B Aca62517 B Abn24508 Aaz99049 AAZ99049 ADQ97596 AAZ57942 AAZ99076 AAC75113 ABN24508 AAS59583 ACF64512 ADA29321 AAF85391 ABK88484 ACA62517 4285 4285 4285 90616 84.4 30.6 30.6 30.6 30.6 29.8 29.8 29.8 50.6 45 5 7 8 9 10 υυ

Aaz99084 Ras targe	Aca52761 Prokarvot		Abv24321 Human pro	Aax58401 Vicia sat	Adj10058 PCR prime	Adj10057 PCR prime	Adj10056 PCR prime	Continuation (2 of	Continuation (2 of	Continuation (2 of	Continuation (2 of	Ads47330 Bacterial	Abd33549 Human can	Aai94947 Human neu	Abt 42823 Human neu	Aat63575 Chicken b	Aaz99087 Ras targe	Adj10059 PCR prime	Aac17425 Human sec	Aaa69206 Bacteriop	Aaa69168 Bacteriop	Aac21986 Human sec	Aah51835 HIV prote
AAZ99084	ACA52761	ABZ15103	, ABV24321	AAX58401	.2 ADJ10058	.2 ADJ10057	.2 ADJ10056	ABX08336_01	.2 ADJ25985 01	.2 ADN97989_01	.2 ADO50281_01	.3 ADS47330	.3 ABD33549	AAI94947	1 ABT42823	AAT63575	AAZ99087	.2 ADJ10059	AAC17425	AAA69206	AAA69168	AAC21986	AAH51835
29	675	2000	1161 5	1665 2	29 1	29 1	29 1	110000 6	11000011	1100001	1100001	1093 1	99291 1	732 4	732 ₿	3791 2	27 3	29 1	208 3	522 3	56506 3	415 3	1116 5
29.0	28.0	28.6	28.3	28.2	28.0	28.0	28.0	28.0	28.0	28.0	28.0	27.8	27.8	27.6	27.6	27.4	27.0	27.0	27.0	. 27.0	27.0	26.8	26.8
500	28.8	28.6	28.2	28.2	28	28	28	28	28	28	28	27.8	27.8	27.6	27.6	27.4	27	27	27	27	27	26.8	26.8
21	27 6	c 24	c 25	c 26	c 27	C 28	c 29	c 30	c 31	c 32	c 33	34	c 35	36	37	c 38	c 39	c 40	c 41	42	43	C 44	45

## ALIGNMENTS

RESULT 1

malignant tumour; signal transmission regulation; cell differentiation; aptamer; inflammation; ss. RNA aptamer #25 for binding Ras target protein. BP AAZ99048 standard; RNA; 100 (first entry) Ras target protein; cell proliferation; Homo sapiens 21-JUN-2000 AAZ99048; AAZ99048 8xxxxxxxxxxxxx

(NISC-) JAPAN SCI & TECHNOLOGY CORP. 98JP-00242596. 98JP-00333284. 99WO-JP004399 WO200009684-A1 14-AUG-1998; 24-NOV-1998; 13-AUG-1999; 24-FEB-2000. 

Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation. WPI; 2000-224330/19.

Sakamoto K;

Yokoyama S, Hirao I,

Claim 6; Page 41; 59pp; Japanese.

The invention relates to novel nucleic acids which bind specifically to the target protein of Ras, e.g. Raf-1. RNA aptamer (AAZ99024-Z99051) based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras target protein and regulating transmission of signal

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Gaps ; 0

Indela

Length 100;

Score 100; DB 12; Pred. No. 2.7e-25;

100.0%; Scc...
100.0%; Pred. No. ...
... 0; Mismatches

Matches 100; Conservative

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Query Match Best Local Similarity

sequence is a synthetic RNA 9A aptamer (100-mer) given in an exemplification of the invention.

8 \$ 3 3 3

Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;

1 GGGAGUGGAGGAAVUCCAUCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAA 60

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This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(1H) - pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxytluorescein, tetramethyl-7-carboxyrhodamine or everse transcription derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as base which is applied as template for the integration of the
                                                                                                                                                 Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating
                                                                                                                              Gaps
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                                                                 Length 100;
                                                                                                                                                                                                                                                                                                                                                                                                                                              ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.
                                                                                                 0; Indels
                             Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;
                                                                                                                                                                                                61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCUUCUGC 100
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causing proliferation or differentiation of cells
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(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                            100.0%; Score 100; DB 3;
100.0%; Pred. No. 2.7e-25;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                 ADJ10063 standard; DNA; 100 BP
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                                                                                                Matches 100; Conservative
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                                                                                Local Similarity
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This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5' substituted-2-oxo(1H)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating
                                                                                                                                                                                                                                                      ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.
                     AUUGGUUUUAGCAVAUGCCUVAGCGACAGCAAGCUUCUGC 100
61 AUUGGUUUUNAGCAUAUGCCUUAGCGACAGCUUCUGC 100
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(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                        Synthetic RNA 9A(5Iy87) aptamer (100-mer).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hirao M, Mitsui T;
                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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the nucleosides

nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, riboxymes and aptamers as reagents or therapeutics in treating disease by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide

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nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, ribozymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA 94 (51947) aptamer (100-mer) given in an exemplification of the invention.
   of the
   which is applied as template for the integration of
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Sequence 100 BP; 25 A; 22 C; 24 G; 0 T; 29 U; 0 Other;

9 9 Gaps ; 0 100.0%; Score 100; DB 12; Length 100; 100.0%; Pred. No. 2.7e-25; ive 0; Mismatches 0; Indels 0 Local Similarity 100. es 100; Conservative Query Match Best Loca Matches a

RESULT 4 ADJ10065

ADJ10065 standard; DNA; 200

(first entry) 17-JUN-2004 Synthetic RNA 2x9A aptamer (200-mer)

ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.

Synthetic.

WO2004007713-A1

22-JAN-2004

28-FEB-2003; 2003WO-JP002342

17-JUL-2002; 2002JP-00208568

(RIKE ) RIKEN KK. (NISC-) JAPAN SCI & TECHNOLOGY CORP

(NISC-) JAPAN SCI & TECHNOLOGY CORP. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Hirao M, Mitsui Hirao I, Yokoyama S,

WPI; 2004-122944/12

Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating

Disclosure; Fig 10; 78pp; Japanese

This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(1H)-pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription 

The invention relates to novel nucleic acids which bind specifically to the target protein of Ras, e.g. Raf-1. RNA aptamer (AAZ99024-Z99051) based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras target protein and regulating transmission of signal causing proliferation or differentiation of cells

Sequence 90 BP; 23 A; 19 C; 22 G; 0 T; 26 U; 0 Other;

Nucleic acid e.g. RNA aptamer capable of binding specifically to trarget protein like Raf-1, useful in drug compositions to treat an diagnose malignant tumors and inflammation.

Claim 6; Page 42; 59pp; Japanese.

ö with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as base which is applied as template for the integration of any of the uncleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, ribozymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids acids are cemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA 2x9A aptamer (200-mer) given in an 9 regulation; Gaps malignant tumour; signal transmission regulation cell differentiation; aptamer; inflammation; ss. ö Length 200; Indels Sequence 200 BP; 50 A; 44 C; 48 G; 0 T; 58 U; 0 Other; 61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCUUCUGC 100 61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCUUCUGC 100 ; Score 100; DB 12; ; Pred. No. 3.4e-25; 0; Mismatches 0; RNA aptamer #27 for binding Ras target protein. Sakamoto K; exemplification of the invention. SCI & TECHNOLOGY 100.0%; 99WO-JP004399 98JP-00242596 98JP-00333284 AAZ99050 standard; RNA; 90 (first entry) Matches 100; Conservative Hirao I, Ras target protein; cell proliferation; WPI; 2000-224330/19 Similarity W02000009684-A1 (NISC-) JAPAN Homo Sabiens. 13-AUG-1999; .4-AUG-1998; 24-NOV-1998; 21-JUN-2000 ZA-PEB-2000. Yokoyama S, AAZ99050; Query Match Local RESULT 5 AAZ99050 888888888888888888 원 ð 셤 

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                                                     GGGAGGGAGAAUUCAUCGAGGAAVAUGUCGACUCCGUCUUCCUUCAAACCAGUAAAAA
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DB 3; Lens.
3. 9e-22;
0; Indels
      Score 90; DB 3
Pred. No. 9e-2
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Best Local Similarity 100.
Matches 90; Conservative
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ADJ10053 standard; RNA; ADJ10053; ADJ1005

17-JUN-2004 (first entry)

ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy. RNA aptamer (RNA9A) SeqID 1 

102004 007713-A1 Unidentified 22-JAN-2004 28-FEB-2003; 2003WO-JP002342.

17-JUL-2002; 2002JP-00208568

(RIKE ) RIKEN KK. (NISC-) JAPAN SCI & TECHNOLOGY CORP. (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.

Hirao M, Mitsui Hirao I, Yokoyama S,

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WPI; 2004-122944/12

Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating diseases

Example 4; SEQ ID NO 1; 78pp; Japanese.

This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(1H)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-postion with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, corporative thereof or a fluorescent molecule selected from fluorescein, 6-carboxyfluorescein, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a cubstituted-2-aminopurin-9-yl group as base which is applied as template for the integration of any of the nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids including antisense DNAs and RNAs, riboxymes and aptamers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification, replication and transcription for their preparation. This polynucleotide sequence is an RNA aptamer (RNASA) given in an exemplification of the invention.

Sequence 98 BP; 24 A; 21 C; 24 G; 0 T; 29 U; 0 Other;

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                                                                    1 GGGAGUGGAGGAAUUC--UGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUAUAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malignant tumour; signal transmission regulation; cell differentiation; aptamer; inflammation; ss.
                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid e.g. RNA aptamer capable of binding specifically to Rae target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation.
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 Length 98;
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3e-18;
hes 0; Indels
                          Indels
                                                                                                         61 AUUGGUUUUNAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 100
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                                                                                                                        59 AUUGGUUUDAGCAUAUGCCUVAGCGACAGCAAGCUUCUGC
Score 84.4; DB 12;
Pred. No. 8.9e-20;
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100.0%; Pred. No. sc.
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24-NOV-1998;
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RESULT 9

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Nucleosides or nucleotides comprising novel base particularly 5-substituted-2-oxo(1H)-pyridin-3-yl group as base, useful in developing functional nucleic acids as reagents or therapeutics in treating
                                                                                   ss; unnatural base; 5'-substituted-2-oxo(1H)- pyridin-3-yl; photoreactive group; biotin; fluorescent molecule; 6-substituted-2-aminopurin-9-yl; aptamer; gene therapy.
                                                                                                                                                                                                                       (RIKE ) RIKEN KK.
(NISC-) JAPAN SCI & TECHNOLOGY CORP.
(ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
                                                                                                                                                                                                                                                             Hirao M, Mitsui T;
                                                                   Synthetic RNA 0C aptamer (100-mer).
                                                                                                                                                                                                                                                                                                                                                Disclosure; Fig 10; 78pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            exemplification of the invention.
          ADJ10066 standard; DNA; 147 BP
                                                                                                                                                                                  28-FEB-2003; 2003WO-JP002342.
                                                                                                                                                                                                     17-JUL-2002; 2002JP-00208568
                                                (first entry)
                                                                                                                                                                                                                                                             Yokoyama S,
                                                                                                                                                                                                                                                                               WPI; 2004-122944/12.
                                                                                                                                           WO2004007713-A1
                                                17-JUN-2004
                                                                                                                                                               22-JAN-2004
                                                                                                                           Synthetie
                             ADJ10066;
                                                                                                                                                                                                                                                             Hirao I,
                                                                                                                                                                                                                                                                                                                              diseases.
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This invention relates to nucleosides or nucleotides that a novel unnatural base, namely the 5'-substituted-2-oxo(IH)- pyridin-3-yl group as a base. Specifically, it refers to nucleic acid molecules integrated with a base substituted at the 5-position with either a photoreactive group (e.g. iodine or bromine), an alkenyl, alkynyl or amino group, biotin or a derivative thereof or a fluorescent molecule selected from fluoresceni, 6-carboxyfluoresceni, tetramethyl-7-carboxyrhodamine or derivatives thereof. The present invention describes preparing nucleic acids by carrying out transcription, replication or reverse transcription with a nucleic acid containing a 6-substituted-2-aminopurin-9-yl group as been which is applied as template for the integration of any of the nucleotides into its complementary position. Accordingly, the nucleosides and nucleotides are useful in developing functional nucleic acids are useful in developing functional nucleic acids ciding antisense DNAs and RNAs, ribozymes and aptemers as reagents or therapeutics in treating diseases by gene therapy. The produced nucleic acids are chemically stable with improved ease of amplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 replication and transcription for their preparation. This polynucleotide sequence is a synthetic RNA OC aptamer (100-mer) given in an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 147 BP; 32 A; 34 C; 37 G; 0 T; 44 U; 0 Other;
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Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
                                                                                                                                             BP
                                                                                                                                           AAC75113 standard; cDNA; 748
                                                                                                                                                                                                    (first entry)
             45; Conservative
Local Similarity
                                                                                                                                                                                                    08-FEB-2001
                                                                                                                                                                        AAC75113;
            Matches
                                                                                                               RESULT 10
                                                                                                                            AAC75113,
                                          ò
                                                                   g
                                                                                                                                                GGGAGUGGAGGAAUUCGAUCGAGGCAUCUGGGAACCCUAUCUUGGUUUGGUAGCUGUAUU 60
                                                                                                                                                                                                    Gaps
                                                                                                                                                                         1,
                                                                                                                                             DB 12; Length 147;
                                                                                                                                                    9e-08;
-hes 24; Indels
                                                                                                                                                                                                                                                             60 AAUUGGUUUUVAGCAUAUGCCUUVAGCGACAGCAAGCUUCUGC 100
                                                                                                                                                                                                                                                                              61 CACCUGUAACAGCAUAVGCCUUAGCGACAGCUACAGCUUCUGC 101
                                                                                                                                                                         0; Mismatches
                                                                                                                                           Score 50.6;
Pred. No. 9e
                                                                                                                                             50.6%;
                                                                                                                                             Query Match
Best Local Similarity 75.2
Matches 76; Conservative
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tumours
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel nucleic acids which bind specifically to represent the sequence of RAS'9076-Z99077) represent the sequence of aptamer inserter that bind the Ras target protein which are used to generate PCR primers. Aptamers based on these sequences are useful in the treatment and diagnosis of malignant tumours and inflammation. The nucleic acids can be used to formulate medicinal compositions that are useful in the treatment of malignant tumours and inflammation and for disease diagnosis by binding specifically to Ras
                                                                                                                                                     protein; malignant tumour; signal transmission regulation; eration; cell differentiation; aptamer; inflammation; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                  Ras target protein-RNA binding sequence #1 for generating primers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 target protein and regulating transmission of signal causing proliferation or differentiation of cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45.0%; Score 45; DB 3; Length 45; 100.0%; Pred. No. 5.9e-06; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAG 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27 AUGUCGACUCCGUCUUCCTUCAAACCAGUUAUAAAUUGGUUUUAG 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human ORFX ORF668 polynucleotide sequence SEQ ID NO:1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 45 BP; 11 A; 10 C; 7 G; 0 T; 17 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 52; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                     (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sakamoto K;
            AAZ99076 standard; RNA; 45 BP
                                                                                                                                                                                                                                                                                                                                                                        98JP-00333284.
                                                                                                                                                                                                                                                                                                                    99WO-JP004399.
                                                                                                                                                                                                                                                                                                                                                     98JP-00242596.
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Hirao I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-224330/19.
                                                                                                                                                         Ras target protein;
cell proliferation;
                                                                                                                                                                                                                                      16200009684-A1
                                                                                                                                                                                                                                                                                                                                                     14-AUG-1998;
24-NOV-1998;
                                                                                                                                                                                                                                                                                                                    13-AUG-1999;
                                                                                   21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            Yokoyama S,
                                                                                                                                                                                                                                                                                 24-FEB-2000
                                                AAZ99076;
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AAZ99076
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RESULT 11 ABN24508/

coagulant; vasotropic; antidiabetic;

us-09-529-397c-25.rng

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antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antianaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft vs host disease; cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS; cholesterol ester storage; systemic lupus erythematosus; infection; alevere combined immunodeficiency; malaria, autoimmune disorder; asthma; allergy; aplastic anaemia; nocturnal heemoglobinuria; burn; wound; hone damage; cartilage damage; antinflammatory disease; coagulation;
           hypotensive; dermatological; immunosuppressive; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and peptides derived from open reading frame useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 1146-1147; 5507pp; English
immunostimulant; thrombolytic;
                                                                                                                                                                                                                                                                99US-0127607P.
99US-0127636P.
99US-0127728P.
                                                                                                                                   thrombosis; contraceptive; ss
                                                                                                                                                                                                                                       31-MAR-2000; 2000WO-US008621
                                                                                                                                                                                                                                                                                           05-APR-1999; 99US-0127728P.
30-MAR-2000; 2000US-00540763.
                                                                                                                                                                                                                                                                                                                                                            Shimkets RA, Leach M;
                                                                                                                                                                                                                                                                                                                                 CURA-) CURAGEN CORP.
                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-602362/57.
                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAB40904
                                                                                                                                                                                   WO200058473-A2
                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                 31-MAR-1999;
                                                                                                                                                                                                                                                                             02-APR-1999;
                                                                                                                                                                                                              05-OCT-2000
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antipsoriatic; antiparkine sum as overceasts; introductive; osteopathic; antipsoriatic; antiparkine sum as overceasts; immunostimulant; cardiant; antiarthritic; immunosuppressant; immunostimulant; cardiant; thrombolytic; coagulant; vancionic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiammatory; antibacterial; antiviral; antifungal; antirheumatic; antithyroid; and antianaemic. The sequences can be used for determining the presence of or predisposition to, or preventing or treating pathological conditions associated with an ORFX-associated disorder. The nucleic acids can be used to express ORFX proteins in gene theretay vectors. The proteins and nucleic acids may be used to treat cancers, proliferative disorders, neurodegenerative disorders mellitue, hypertension, hypothyroidism, cholesterol ester storage, systemic lupus erythematosus, severe combined immunodeficiency (SCID), AIDS, viral; bacterial or fungal infection, malaria, autoimmune cationare, asthma, allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, nocturnal haemoglobinutia, autiinfammatory disease; to enhance coagulation; to inhibit thrombosis; and as a contraceptive AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, which represent the human ORFX open reading frames 1 to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary;

Sequence 748 BP; 134 A; 218 C; 221 G; 174 T; 0 U; 1 Other;

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18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG 77
                           Gaps
                          .
0
Score 30.6; DB 3; Length 748; Pred. No. 1.7;
                          29; Indels
                          12; Mismatches
 30.6%;
                          36; Conservative
               Local Similarity
                                                                            317
   Query Match
                            Matches
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Best Local Similarity Query Match CCCTGGGCACGGGAAGC 241

94

CCUUAGCGACAGCAAGC

78

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Treferred to as open reading frame, ORFX, where X is 1-11491 (see Table 1 in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX in the specification). ABN15762 to ABN2752 encode the human ORFX in the manning a pathology associated with an ORFX-associated disorder in humans, and in the manufacture of a medicament for treating a syndrome associated with ORFX-associated disorder. ORFX polymucleotide syndrome associated with ORFX-associated disorder. ORFX polymucleotide sequences can be used in gene therapy. ORFX sequences can be used in the treatment of cancer, hyperproliferative disorders, cirrhosis of liver, psoriasis, benign tumours, keloid, degenerative disorders; haemorrhage, osteoarthis, neurodegenerative disorders, disorders related to organ transplantation, cardiovascular diseases, disorders; haemorrhage, osteoarthis, neurolosis mumune disorders; hypothyroidism, cholesterol ester storage disease, autoimmune disorders such as multiple societos; rheumatoid arthritis, autoimmune inflammatory eye disease. ORFX proteins are also disease and autoimmune inflammatory eye disease. ORFX proteins are also useful for treating burns, incisions, ulcers, for treating osteoporosis, bone degenerative disorders, or periodontal disease, and for gut protection or regeneration and treatment of lung or liver fibrosis, cepertusion njury in various tissues and conditions resulting from systemic cytokine damage. NB. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/published\_pot\_sequences Human; open reading frame; ORFX; gene therapy; cancer; cirrhosis; hyperproliferative disorder; psoriasis; benign tumour; haemorrhage; degenerative disorder; osteoarthritis; neurodegenerative disorder; cardiovascular disease; diabetes mellitus; systemic lupus erythematosus; hypertension; hypothyroidism; cholesterol ester storage disease; immune deficiency; immune disorder; infectious disease; autoimmune disorder; rheumatoid arthritis; autoimmune thyroiditis; present invention describes substantially purified human proteins Novel human polypeptides and polynucleotides useful for diagnosing, preventing and treating cardiovascular disease, neurodegenerative, hyperproliferative disorders and autoimmune disorders. 30.6%; Score 30.6; DB 6; Length 748; 46.8%; Pred. No. 1.7; Sequence 748 BP; 134 A; 218 C; 221 G; 174 T; 0 U; 1 Other; Human ORFX polynucleotide sequence SEQ ID NO:17493. Disclosure; SEQ ID NO 17493; 1037pp; English. ABN24508 standard; cDNA; 748 BP 29-MAY-2001; 2001WO-US010836. 2000US-0206132P. 2000US-0228716P. myasthenia gravis; gene; ss. (first entry) Shimkets RA, Leach MD; (CURA-) CURAGEN CORP. 2002-106308/14. P-PSDB; ABP08756. WO200192523-A2 Homo sapiens. 30-MAY-2000; 29-AUG-2000; 24 - JUN - 2002 06-DEC-2001 ABN24508; 

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equences AASSTONG-AASSTONG TEPPEBBLE DATE MAY MORECULES UNCOLDED SEQUENCES AASSTONG-AASSTONG TEPPEBBLE DATE MAY MORECULES UNCOLDED SECONDATIONS caused in the treatment, prevention and diagnosis of medical conditions caused by P. acnes. The disorders include SAPHO syndrome (synovitis, acne, pustulosis, hypertosis and osteomycalitis), uveltis and endophibalmitis. P. acnes is also involved in infections of bone, joints and the central nervous system, however it is particularly involved in the inflammatory lesions associated with acne vulgaris. A method for detecting the presence or absence of P. acnes in patient comprises contacting a sample with a binding agent that binds to the proteins of the invention and determining the amount of bound protein in the sample. The polypeptides may be used as antigens in the production of antibodies specific for P. acnes proteins. These antibodies can be used to downregulate expression and activity of P. acnes polypeptides and therefore treat P. acnes intections. The antibodies may also be used as diagnostic agents for determining P. acnes presence, for example, by enzyme linked immunosorbent assay (ELISA). This sequence encodes the sequence data for this patent did not form part of the printed specification, but was obtained in alectronic format directly from WIPO at the vipo.int/pub/published_pct_sequences
  ö
                                                          77
                                                                                                                                                                                                                                                                                                                                                                                                      SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis; uveitis; endophthalmitis; bone; joint; central nervous system; ELISA; inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay; dermatological; osteopathic; neuroprotectant; ds.
                                    18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Propionibacterium acnes polypeptides and nucleic acids useful for vaccinating against and diagnosing infections, especially useful for treating acne vulgaris.
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0
                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes immunogenic protein encoding DNA #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequences AAS59506-AAS59804 represent DNA molecules encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bhatia A;
  Indels
  29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mitcham JL, Wang SS, Jen S, Carter D;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 78; 1069pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Skeiky YAW, Persing DH, Mitcham JI
L'maisonneuve J, Zhang Y, Jen S,
                                                                                                                                                                                                                                                     AASS9583 standard; DNA; 15776 BP
12;
                                                                                                                                                     257 cccresecaceseasic 241
                                                                                                                  94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-APR-2001; 2001WO-US012865.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-APR-2000; 2000US-0199047P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-JUN-2000; 2000US-0208841P.
                                                                                                                  CCUUAGCGACAGCAAGC
                                                                                                                                                                                                                                                                                                                                13-FEB-2002 (first entry)
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-616774/71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200181581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-2001.
36;
                                                                                                                                                                                                                                                                                          AAS59583;
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  Matches
                                                                                                                                                                                                             RESULT 12
                                                                                                                                                                                                                                   AAS59583
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The invention relates to an isolated polymucleotide (ACF64415-ACF64733)

concoding a Propionibacterium acnes protein. The invention also relates to polymebrides encoded by the polymucleotides (ABM35624-ABM64536) and to immunogenic fragments of P. acnes polypeptides. The invention additionally encompasses expression vectors and host cells comprising a polymetheotide of the invention, antibodies against polypeptides of the invention are comprising a polymethide of the invention; and this method for stimulating an immune response specific for a P. acnes to olypeptide and an isolated T cell population comprising T cells prepared via this method; a vaccine composition (comprising P. acnes polymethides, polymethides, antibodies, fusion proteins, T cell populations, or attigen-presenting cells that express the polymethide); a method and kit for detecting or determining the presence of P. acnes in a content of the method for inhibiting the development of P. acnes in a patient; and a method for inhibiting the development of P. acnes in a protein, T cell populations or antigen-presenting cells that express the polymeptides are useful for diagnosing, preventing or treating acnes protein; The polymulations an immune response specific for a P. acnes protein. The polymulating an immune response specific for a P. acnes protein; The polymulations an immune response specific for a P. acnes protein; The polymulations and immune response specific for a P. acnes cucle contecting an immune response as probes or primers for nucleic acid hybridisation. The vaccine composition is useful for the stimulation of an immune response against P. acnes, or for treating acne, attimulating acids and also be used as probes or primers for a timulation of an immune response against P. acnes, or for treating acne,
                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Propionibacterium acnes polypeptides and polynucleotides encoding the polypeptide, useful for diagnosing, preventing or treating acne vulgaris, or for stimulating an immune response specific for a P. acnes protein.
                                                                                                                                          11
                                                                                                                                          18 UCGAGGCAUAUGUCGACUCCGUCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG
                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Maisonneuve JL;
Jones R, Carter D;
Sequence 15776 BP; 3393 A; 4931 C; 4483 G; 2969 T; 0 U; 0 Other;
                                          30.6%; Score 30.6; DB 4; Length 15776; 46.8%; Pred. No. 4.5; ive 12; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Acne vulgaris, antiseborrhoeic, dermatological, antibacterial, immunostimulant, immune response, vaccine, ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Skeiky YAW, Persing DH, Bhatia A,
ng S, Jen S, Lodes MJ, Benson DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Propionibacterium acnes DNA contig sequence #78.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 78; 1481pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                          ACF64512 standard; DNA; 15776 BP.
                                                                                                                                                                                                                                                                                     8487 CCCTGGGCACGGAAGC 8503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang S, Jen S, Lode
Vallieve-Douglass J;
                                                                                                                                                                                                                                        78 CCUUAGCGACAGCAAGC 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-OCT-2002; 2002WO-US032727.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-OCT-2001; 2001US-00978825.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                            30.6
Best Local Similarity 46.8
Matches 36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Propionibacterium acnes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2003-381789/36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003033515-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24-APR-2003
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Barth B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACF64512;
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and the kit is useful for performing a diagnostic assay.

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Homo sapiens.
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                                                                                                                                                                                   21-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                tokoyama S,
                                                                                                                                                                                                                                                                                                            24-FEB-2000
                                                                                                                                                            AAZ99049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                              RESULT 15
AAZ99049
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New Acinetobacter baumanii proteins and nucleic acids, useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, or as biocontrol agents for
                                                                                                                                      77
          sequence represents a P. acnes DNA contig which is specifically claimed in the invention. Note: The sequence date for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention relates to isolated Acinetobacter baumannii nucleic acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The A. Daumanni nucleic acids and polypeptides are useful as reagents for diagnosing a bacterial disease, as components of antibacterial vaccines, as targets for antibacterial drugs, to detect the presence of A. baumannii and other Acinetobacter species in a sample, in screening compounds for the ability to interfere with the A. baumannii life cycle or to inhibit A. baumannii infection, and as biocontrol agents for
                                                                                                                                      18 UCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                     ds; gene; Acinetobacter baumannii; bacterial disease; antibacterial; vaccine; plant biocontrol agent.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plants. The present sequence represents DNA encoding an A. baumannii
                                                                   Sequence 15776 BP; 3393 A; 4931 C; 4483 G; 2969 T; 0 U; 0 Other;
                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
                                                                                       Length 15776;
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                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 366 BP; 131 A; 65 C; 63 G; 107 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                  DNA encoding Acinetobacter baumannii protein #608.
                                                                                                               29;
                                                                                         DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 30.4%; Score 30.4; DB 9; Similarity 39.8%; Pred. No. 1.7; 35; Conservative 17; Mismatches 36;
                                                                                                    4.5;
                                                                                                               12; Mismatches
                                                                                         30.6%; Score 30.6;
46.8%; Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example; SEQ ID NO 608; 328pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (GENO-) GENOME THERAPEUTICS CORP.
                                                                                                                                                                                                                                                               ADA29321 standard; DNA; 366 BP
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                                                                                                                                                                                  CCUUAGCGACAGCAAGC
                                                                                                                                                                                                CCCTGGGCACGGGAGC
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                               36; Conservative
                                                                                                                                                                                                                                                                                                                                                                                          Acinetobacter baumannii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-576092/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 35; Conserv
                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bush D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; ADA33447.
                                                                                                                                                                                                                                                                                                            20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                             04-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-JUN-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      13-MAY-2003.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Breton G,
                                                                                                                                                                                                                                                                                     ADA29321;
                                                                                                                                                                                78
                                                                                                                                                           8427
                                                                                                                                                                                                        8487
                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plants.
                                                                                                               Matches
                                                                                                                                                                                                                                        RESULT 14
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101 GGGTGTTTATGAATATAGCTTTCTATATGTCGCACCAGTAATTGTGCGAAGAAGTAATAG 42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    malignant tumour; signal transmission regulation; cell differentiation; aptamer; inflammation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acid e.g. RNA aptamer capable of binding specifically to Ras target protein like Raf-1, useful in drug compositions to treat and diagnose malignant tumors and inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30.0%; Score 30; DB 3; Length 98;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 AUUGGUUUUAGCAUAUGCCUUAGCGACAGCAAGCUUCUGC 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 98 BP; 24 A; 24 C; 26 G; 0 T; 24 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RNA aptamer #26 for binding Ras target protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                      :||::: || :|: || TCTGGTTTATGCGTATATTCTAGATTCA 14
                                                                  61 AUUGGUUUUAGCAUAUGCCUUAGCGACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Search completed: April 19, 2005, 16:27:31
Job time : 432 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (NISC-) JAPAN SCI & TECHNOLOGY CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sakamoto K;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 6; Page 41; 59pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99WO-JP004399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98JP-00242596,
98JP-00333284,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        63.0%;
                                                                                                                                                                                                                                                                                         AAZ99049 standard; RNA; 98
                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hirao I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     target protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200009684-A1.
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Sequence 324279, Sequence 324280, Sequence 790, App Sequence 130987, Sequence 150280, Sequence 14431, A

US-10-322-281-744
US-10-479-081-104
US-10-479-081-104
US-10-097-111-10
US-10-321-111-10
US-10-321-111-10
US-10-321-111-10
US-10-321-35948
US-10-052-482-85
US-10-052-482-199104
US-10-027-632-199104
US-10-027-632-199104
US-10-027-632-324279
US-10-027-632-324280
US-10-027-632-324279
US-10-027-632-324279
US-10-027-632-324279
US-10-027-632-324280
US-10-027-632-324280
US-10-027-632-324280
US-10-027-632-324280
US-10-027-632-324280
US-10-027-632-324280
US-10-027-632-14431
US-10-027-632-14431
US-10-027-632-110124
US-10-027-632-110124
US-10-027-632-110124
US-10-027-632-110124
US-10-027-632-110124
US-10-027-632-110124
US-10-027-632-110124

Sequence 15351, A Sequence 324279, Sequence 324280, Sequence 199104, Sequence 199104,

Sequence Sequence Sequence Sequence

522 56506 1116 1884 48995

Sequence 162, App Sequence 162, App Sequence 310, App Sequence 73812, A Sequence 73810, A Sequence 73810, A

US-10-329-624-162 US-10-425-115-310 US-10-437-963-73812 US-10-470-048B-23 US-10-437-963-73810 US-10-437-963-73813

1165 1550 2427 2577 2688

ALIGNMENTS

Sequence 14431, A Sequence 14432, A Sequence 101724, Sequence 101724, Sequence 13160, A Sequence 1380, Ap Sequence 24541, A

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LENGTH: 4285
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US-10-104-580-1
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Best Local Si
Matches 27;
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Sequence 2908, Ap
Sequence 2908, A
Sequence 24310, A
Sequence 13576, A
Sequence 12523,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Appli
Sequence 1, Appli
Sequence 25760, A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1, Appli
Sequence 40631, A
                                                                                                                April 19, 2005, 13:28:09; Search time 5352 Seconds (without alignments) 113.354 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
                                                                                                                                                                                                                          1 gggaguggaggaauucaucg.....uagcgacagcaagcuucugc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Published Applications NA:*

(cgn2 6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
(cgn2 6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO6_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO8_NEW_PUB.seq:*
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(cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO9_NEW_PUB.seq:*
(cgn2 6/ptodata/2/pubpna/USO08_PUBCOMB.seq:*
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                 version 5.1.6
- 2005 Compugen Ltd.
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10S-09-38-842A-2908

10S-09-938-842A-2908

10S-09-938-842A-2908

1 US-09-938-842A-2908

1 US-01-357-930-24310

8 US-10-357-930-24310

8 US-10-425-115-121623
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US-10-419-723-1
US-10-369-493-25760
                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                         5622541 seqs, 3033355566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                  nucleic search, using sw model
                                                                                                                                                                                                                                                       IDENTITY NUC
Gapop 10.0 , Gapext 1.0
                GenCore
Copyright (c) 1993
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118
114
117
                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 2000000000
                                                                                                                                                                                   US-09-529-397C-25
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1691139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query
Match
                                                                                                                                                                                                                                                       Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Perfect score:
                                                                                  OM nucleic -
                                                                                                                                                                                                                          Sequence:
                                                                                                                                                                                                                                                                                                            Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Database
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                                                                                                                                                  Length 4285;
                                                                                                                                                              Indels
                                                                                                                                                  DB 14;
                                                                                                                        ; TYPE: DNA
; ORGANISM: Populus balsamifera subsp. trichocarpa
US-10-104-580-1
                                                                                                                                                29.8%; Score 29.8; D
33.3%; Pred. No. 11;
tive 22; Mismatches
                                                                                                                                                                                                    UNAGCAUAUGCCUUAGCGACA 88
                                                                                                                                                              Conservative
                                                                                                                                                      Local Similarity
nes 27; Conserv
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US-09-938-842A-2908
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: AL, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR PILING DATE: 2000-03-21
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-23
PRIOR PELING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-09-06
PRIOR PILING DATE: 2000-10-23
PRIOR PILING DATE: 2000-11-23
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-11-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2000-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-12-22
PRIOR PILING DATE: 2001-02-65
PRIOR FILING DATE: 2001-02-66
PRIOR FILING DATE: 2001-02-66
PRIOR FILING DATE: 2001-02-66
PRIOR PILING DATE: 2001-02-66
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                                                                                                                                                                                  Sequence 40631, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Haselbeck, Robert
APPLICANT: Ohleen, Kari
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 2908, Application US/09938842A
Patent No. US20020160378A1
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
Zyskind, Judith
Wall, Daniel
Trawick, John
Carr, Grant
Yamamoto, Robert
Forsyth, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | ::
GATT 500
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US-09-938-842A-2908/c
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Sequence 2908, Application US/09938842A

Sequence 2908, Application US/09938842A

PUBLICANT: Harper, Jeff

APPLICANT: Harper, Jeff

APPLICANT: Kreps, Joe1

APPLICANT: Zhu, Tong

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

TITLE OF INVENTION: SAME, AND METHODS OF USE

FILE REPERENCE: SCRIP1300-3

CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT APPLICATION NUMBER: US 60/227,866

PRIOR PILING DATE: 2001-08-24

PRIOR FILING DATE: 2001-01-16

SEQ ID NO 2908

SEQ ID NO 2908

LINGTH: 2000

MENTING DATE: 2000

LINGTH: 2000

LINGTH: 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 28.6%; Score 28.6; DB 9; Length 2000; Best Local Similarity 35.8%; Pred. No. 21; Matches 24; Conservative 19; Mismatches 24; Indels 0;
                                                                                                                                                                                                                                                                                                                                       ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-2908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 28.69
Best Local Similarity 35.89
Matches 24; Conservative
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699 GTTTTTA 693
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699 GTTTTTA 693
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; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1, 2, 3
; CTHER INFORMATION: n = A,T,C or G
US-10-357-930-24310
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ORGANISM: Zea mays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-10-767-701-13576/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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                                                               Sequence 30801, Application US/10425114

Publication No. US20040034888A1

Sequence 30801, Application US/10425114

SEQUENCE INCORNATION:

APPLICANT: Liu, Jingdong

APPLICANT: Screen, Steven E

APPLICANT: Screen, Steven E

APPLICANT: Cao, Yongwei

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With

TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

TITLE OF INVENTION: NUMBER: US/10/425,114

CURRENT APPLICATION NUMBER: US/10/425,114

CURRENT PILING DATE: 2003-04-28

SEQ ID NO 30801

LENGTH: 586
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPOSITIONS, KITS, AND METHODS FOR ION, ASSESSMENT, PREVENTION, AND THERAPY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92 GGGGCATTTTTATGTTGTTATTAGATTCTCTCCTGCTCCACCGCCATCATAACTCGGTT 33
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Clone ID: UC-ZMFLB73080F09_FLI
US-10-425-114-30801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 24310, Application US/10357930
; Publication No. US20040259086A1
GENERAL INFORMATION:
APPLICANT: Schlegel. Robert
APPLICANT: Endege, Wilson
APPLICANT: Endege, Wilson
APPLICANT: Monahan, John
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
TITLE OF INVENTION: HUMAN PROSTATE CANCER
CURRENT APPLICATION NUMBER: US/10/357,930
CURRENT FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: 60/183,319
PRIOR FILING DATE: 2000-03-16
PRIOR APPLICATION NUMBER: 60/219,314
PRIOR FILING DATE: 2000-05-19
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
PRIOR FILING DATE: 2000-07-18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 62232
SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Zea mays FEATURE:
                                                       US-10-425-114-30801/c
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Sequence 121623, Application US/10425115
| Publication No. US20040214272A1
| Publication No. US20040214272A1
| Publication No. US20040214272A1
| GENERAL INFORMATION:
| APPLICANT: La Rosa, Thomas J.
| APPLICANT: Cao, Yongwei
| APPLICANT: Chou, Yihua APPLICANT: Cao, Yongwei
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: Plants
| TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With TITLE OF INVENTION: NumBER 02102220 B
| CURRENT APPLICATION NUMBER: 2003-04-28
| CURRENT PILING DATE: 2003-04-28
| SEQ ID NOS: 369326
| SEQ ID NO 121623
| LENGTH: 1851
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Other Molecules Associated With
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8 GAGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCAAACCAGUUAUAAAUUGGUU 67
                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Shou, Yihua
APPLICANT: Cao, Yihua
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Asso
TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement FILE REFERENCE: 38 -21 (53535) B
CURRENT APPLICATION NUMBER: US/10/767,701
CURRENT FILING DATE: 2004-01-29
NUMBER OF SEQ ID NOS: 63128
SEQ ID NO 13576
LENGTH: 1612
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28.2%; Score 28.2; DB 18; Length 1612;
Best Local Similarity 38.2%; Pred. No. 27;
Matches 34; Conservative 17; Mismatches 38; Indels 0;
      Length 1161;
                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: Clone ID: SORBI-28MAY03-CLUS1303_1
US-10-767-701-13576
Query Match 28.2%; Score 28.2; DB 18; Best Local Similarity 37.1%; Pred. No. 24; Matches 33; Conservative 18; Mismatches 38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Sorghum bicolor
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us-09-529-397c-25.rnpb

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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-419-723-1
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                                                                                                                                                                                               12 AAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 28.0%; Score 28; DB 14; Length 1691139; 1 Similarity 41.7%; Pred. No. 4e+02; 25; Conservative 15; Mismatches 20; Indels 0;
                                                                                                                                               .;
0
                                                                                               Length 1851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Greetsedettir, Solveig
APPLICANT: Greetsedettir, Sif
APPLICANT: Greetsedettir, Sif
APPLICANT: Horleifsson, Gudmar
APPLICANT: Reynisdettir, Sigridur Th.
APPLICANT: Glicher, Jeffrey
TITLE OF INVENTION: SUSGEPTIBILITY GENE FOR HUMAN STROKE;
TITLE OF INVENTION: METHODS OF TREATMENT
FILE REFERENCE: 2345.2010-005
CURRENT APPLICATION NUMBER: 10/255,120
PRIOR FILING DATE: 2002-09-25
PRIOR APPLICATION NUMBER: 10/055,120
PRIOR APPLICATION NUMBER: 10/055,120
PRIOR APPLICATION NUMBER: 10/055,120
PRIOR APPLICATION NUMBER: 10/0575,14
PRIOR APPLICATION NUMBER: 2002-02-03
PRIOR APPLICATION NUMBER: 2001-03-19
                                                                                                                                                  Indels
                                                                                                  DB 18;
                      ; OTHER INFORMATION: Clone ID: MRT4577_42398C.1 US-10-425-115-121623
                                                                                          Ouery Match 28.2%; Score 28.2; DB
Best Local Similarity 37.1%; Pred. No. 29;
Matches 33; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                        1273 CCAGCAAGCGCATTAGGGAAAGGAAGGATT 1245
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1. Application US/10067514
Publication No. US20030054531A1
GENERAL INFORMATION:
APPLICANT: Gretaredottir, Solveig
APPLICANT: Jonsdottir, Sigridur Th.
TITLE OF INVENTION: HUMAN STROKE.GENE
TITLE REFERENCE: 2345.2010-003
CURRENT FILING DATE: 2002-02-04
PRIOR APPLICATION NUMBER: US/10/067,514
CURRENT FILING DATE: 2002-03-04
PRIOR PILING DATE: 2001-03-19
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                               68 UUAGCAUAUGCCUUAGCGACAGCUU 96
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/10419723; Publication No. US20040014099A1; GENERAL INFORMATION:
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1691139
                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
US-10-067-514-1/c
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APPLICANT: Cao, Yongwei
APPLICANT: Cao, Yongwei
APPLICANT: Hinkle, Gregory J.
APPLICANT: Stater, Steven C.
APPLICANT: Stater, Steven C.
APPLICANT: Gldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROPERTIES
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REPERENCE: 38-10(52052)
CURRENT APPLICATION NUMBER: US/10/369,493
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR FILING DATE: 2002-02-21
                                                                                                                                                   127542 AGTTGATCCATGCTTTTGGAGGAGGAGCTTATCCCTTCAAAGCAGTAATAAAAGTGTTTTAG 127483
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  Length 1691139;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 744, Application US/10322281

Sequence 744, Application US/10322281

Publication No. US20040126762A1

GENERAL INPORMATION:

APPLICANT: David W. Morris

APPLICANT: Marc S. Malandro

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

TITLE OF INVENTION: Novel Compositions and Methods in Cancer

CURRENT APPLICATION UNMBER: US/10/322,281

CURRENT FILING DATE: 2002-12-17

NUMBER OF SEQ ID NOS: 866

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 744

LENGTH: 99291
28.0%; Score 28; DB 17; Length 16
41.7%; Pred. No. 4e+02;
tive 15; Mismatches 20; Indels
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                                                                                                                                                                                                                                                                                     US-10-369-493-25760

Sequence 25760, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Schizosaccharomyces pombe
  Query Match
Best Local Similarity 41.74
Matches 25; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 25760
LENGTH: 1093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 GTTTGTTCTAT 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         64 GGUUUUAGCAU 74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
CORGANISM: Homo sapiens
US-10-322-281-744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-10-322-281-744/c
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GENERAL INFORMATION:
APPLICANT: PELETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: GROS, PHILLIPPE
TITLE OF INVENTION: BACODE ANTI-MICROBIAL POLYPEPTIDES
TITLE OF INVENTION: BACODE ANTI-MICROBIAL POLYPEPTIDES
TITLE OF INVENTION: BACODE ANTI-MICROBIAL POLYPEPTIDES
TITLE OF INVENTION NUMBER: US/10/097,111
CURRENT APPLICATION NUMBER: 09/76,412
PRIOR PAPLICATION NUMBER: 09/76,412
PRIOR PLING DATE: 1000-09-29
PRIOR PLING DATE: 1099-09-30
PRIOR PLING DATE: 1999-09-30
NUMBER OF SEQ ID NOS: 552
SOFTWARE: PARENTIN VOY: 2.1
SEQ ID NO 479
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                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                           Query Match 27.6%; Score 27.6; DB 19; Best Local Similarity 47.6%; Pred. No. 33; Matches 39; Conservative 9; Mismatches 34;
                                    FEATURE:
NAME/KEY: misc feature
LOCATION: (711).
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
LOCATION: (732)...(732)
OTHER INFORMATION: n is a, c, g, or t
FEATURE:
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FEATURE:
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ORGANISM: Streptococcus pneumoniae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 10, Application US/10097111; Publication No. US20030138771A1; GENERAL INFORMATION: APPLICANT: PELLETIER, JERRY
APPLICANT: GROS, PHILLIPPE
APPLICANT: DUBOW, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; Sequence 47, Application US/10097111; Publication No. US20030138771A1
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                                                                                                                                                                                                                  ; OTHER INFORMATION: nbla-03439-f
US-10-479-081-104
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246 AATGCAGTTGACAC 260
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  LOCATION: (706)..(706)
OTHER INFORMATION: n is a,
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US-10-097-111-10
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TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED FROM NEUROBLASTOMA
TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED FROM NEUROBLASTOMA
TITLE OF INVENTION: NUCLEIC ACIDS ISOLATED FROM NEUROBLASTOMA
FILE REFERENCE: 7388-80893
CURRENT APPLICATION NUMBER: US/10/479,081
CURRENT FILING DATE: 2003-11-26
PRIOR FILING DATE: 2002-05-30
PRIOR FILING DATE: 2001-05-31
PRIOR FILING DATE: 2001-05-31
PRIOR APPLICATION NUMBER: JP 2001-155260
PRIOR FILING DATE: 2001-06-34
NUMBER OF SEQ ID NOS: 742
SOFTWARE: PALENTIN VENESION 3.2
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; Sequence 104, Application US/10479081
; Publication No. US20050059001A1
; GENERAL INFORMATION:
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THER INFORMATION: n is a,
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LOCATION: (87)...(87)
OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
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OTHER INFORMATION: n is a,
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THER INFORMATION: n is a,
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LOCATION: (90)...(90)
OTHER INFORMATION: n is a,
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NAME/KEY: misc feature
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OTHER INFORMATION: n is a,
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OTHER INFORMATION: n is a,
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LOCATION: (4)...(4)
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NAME/KEY: misc_feature
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JOCATION: (650)..(650)
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LENGTH: 732
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; TITLE OF INVENTION: DNA SEQUENCES FROM S. PNEUMONIAE BACTERIOPHAGE EP1 THAT
; TITLE OF INVENTION: ENCODE ANTI-MICROBIAL POLYPEPTIDES
; FILE REFERENCE: 07346-0603
; CURRENT APPLICATION NUMBER: US/10/097,111
; CURRENT FILING DATE: 2002-07-24
; PRIOR PILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/157,218
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 552
; NUMBER OF SEQ ID NOS: 552
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 56506
; TYPE: DNA
; ORGANISM: Streptococcus pneumoniae
US-10-097-111-10

QUETY MATCh
Best Local Similarity 40.0%; Pred. No. 2.7e+02;
MATCHES 30; CONSELVATIVE 15; Mismatches 30; Indels 0; Gaps 0;
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6 B 6

Search completed: April 19, 2005, 15:28:25 Job time : 5357 secs

BP051024 hz76e08.b

AQ955733 BP051024 CB094897

BZ891642

CC115139

B0172B04-B0161F04-B0175H04-

CA892404 CA890800 CA892977 AG525698

Mus muscu 602411369

UI-M-FRO-

Bn01b\_03j BW594105 BW545837 CH240\_325

BG393101 BU708057 CC491386 CC868108 BW594105 BW545837 BQ531573 CF791691 BG649176

BQ531573 APEX2 5 F BQ531573 APEX2 5 F BQ531501 APEX3 35 CF791691 880034 MA BG649176 EM1 77 E0 BE363373 WS1 62 B0

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Run

Sequence:

Minimum DB Maximum DB

Database

Result

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Searched:

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Fax: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=PM2-HT0224-291
099-002-c00&t3=1999-10-29&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 17
High quality sequence start: 17
High quality sequence stop: 415.
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1 (bases 1 to 642)
1 (bases 2 to 642)
1 (bases 2 to 642)
1 (bases 3 to 642)
1 (bases 3 to 642)
1 (bases 4 to 642)
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1 (bases 7 to 642)
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Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000) 20202663
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/organism="Homo sapiens"
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BG393101
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VERSION
KEYWORDS
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AUTHORS
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                                                                                                               April 19, 2005, 13:28:09 ; Search time 3095 Seconds (without alignments) 1229.863 Million cell updates/sec
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CN553289
CN226782
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BU209960
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                  version 5.1.6
- 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
                                                                                 nucleic search, using sw model
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seq length: 200000000
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/dow\_stage='Adult"
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Site\_2: Smal; A mini-library was made by cloning products

BZ944697 CH240 121 CN464219 7866.1 Af CA249294 SCSBFL110 CE114143 tigr-gss-

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1-7-22 Suehirro-chou, Taurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:hattori@gsc.riken.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availablity, please contact Kuniya Abe (abe@rtc.riken.jp).
Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1
Koyadai, Tsukuba, 305-0074 Japan
phone: 81-298-36-9189, fax: 81-298-36-9199
e-mail: abe@rtc.riken.jp
derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the PUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under low stringency conditions."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG557770 149 bp DNA linear GSS 05-JUN-2004
Mus musculus molossinus DNA, clone:MSMg01-476B14.T7, genomic survey
                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                      12 AAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCAAACCAGUUAUAAAUUGGUUUUAG 71
                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
BAC end Sequences of Library MSMg01
Unpublished
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Direct Submission
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0
                                                                                                                                                          34.6%; Score 34.6; DB 2; Length 642; 37.0%; Pred. No. 0.71; tive 22; Mismatches 29; Indels
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/clone_lib="MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mus musculus molossinus"
/mol_type="genomic DNA"
/gub_species="molossinus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:57486"
/clone="MSMg01-476B14.T7"
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                                                                                                                                                                                                                                                                                                                                                                         210 AATTTGCGTTTACAACAA 230
                                                                                                                                                                                                                                                                                                                                           72 CAUAUGCCUUAGCGACAGCAA 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AG557770
AG557770.1 GI:48318468
GSS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus molossinus
Mus musculus molossinus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 749)
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Best Local Similarity 51.09
Matches 25; Conservative
                                                                                                                                                                                                       30; Conservative
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LIBRARY
                                                                                                                                                                                    Best Local Similarity
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R.Site 2
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KEYWORDS
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AG557770/c
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(http://www.jax.org/resources/documents/dhares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polymucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWADA2 (gil 47721141gbl AT29072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli KL10-Gold (Stratagene) cells and selected for ampicillin resistance."
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/clone lib="Mouse 10kb plasmid UGGCM library"
/note="Vector: PWD47Dv; Purified genomic DNA from M.musculus C57BL/GJ (female) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 442)
Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,
                                                                                                                                                                     AZ955882
2M0222110F Mouse 10kb plasmid UUGC2M library Mus musculus genomic
clone UUGC2M0222110 F, genomic survey sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R. Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah
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Query Match 31.2%; Score 31.2; DB 8; Length 442; Best Local Similarity 32.6%; Pred. No. 9.8; Matches 30; Conservative 24; Mismatches 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rm. 308, Biomedical Polymers Research Bldg., 20
84112, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0222 row: I column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seg primer: CGTTGTAAAACGACGCCAGTClass: plasmid ends
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="genomic DNA"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'db xref="taxon:10090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              clone="UUGC2M0222110"
                                                                                                                                                                                                                                                                                                                                                          Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                AZ955882.1 GI:13827109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 801 585 5606
Fax: 801 585 7177
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KEYWORDS
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AZ955882
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Matches 29; Conserve
                                                                                   Rattus.
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AMGNNUC:MRBE4-00015-C9-A rat brain E15 (10375) Rattus norvegicus
cDNA clone mrbe4-00015-c9 5', mRNA sequence.
CB736914 GI:29804127
                                                                                                                                                                             B21536 696 bp DNA linear GSS 16-SEP-1997 F21F23-T7 IGF Arabidopsis thaliana genomic clone F21F23, genomic
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                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 696)
Peng, J., Dewar, K., Buehler, E., Kim, C., Li, Y., Shinn, P., Sun, H. and
                 9 AGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUU 68
 /sex="hermaphrodite"
/clone_lib="IGF"
/note="Vector: BeloBACII; Site_1: EcoRI; Site_2: EcoRI;
Produced by Thomas Altmann"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dept. of Biology, University of Pennsylvania, Philadelphia, PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
                                                                                 332 TITITGTTTTTGTTTTTCGAGACCAGGTTTCT 363
                                                                67 UUUAGCAUAUGCCUUAGCGACAGCAUCU 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jecker@atgenome.bio.upenn.edu
Seg primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis Thaliana Genome Center
University of Pennsylvania
                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
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High quality sequence stop: 143.
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/ecotype="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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Unpublished (1997)
Other_GSSs: F21F23-Sp6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="F21F23"
                                                                                                                                                                                                                             B21536
B21536.1 GI:2396590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rel: 215-898-9384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 215-898-8780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            969. .1
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                                                                                                                                                                                                                   survey sequence.
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CB736914/c
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1074 bp mRNA linear EST 21-JUL-2000 60121621F1 NCI_CGAP_Lu29 Mus musculus cDNA clone IMAGE:3586661 5', BE371824
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: ggapbs-r@mail.nih.gov
Tisaue Procurement: Gilbert Smith, Ph.D.

Tisaue Procurement: Gilbert Smith, Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM8748 row: j column: 06

High quality sequence stop: 380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67
                         Rattus norvegicus
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="mxbe4-00015-c9"
/tissue_type="brain B15"
/clone_lib="rat brain B15 (10375)"
/note="Vector: pBCB; Site_1: BstXI; Site_2: Not1; rat
brain B15"
                                                                                                                          Amgen EST Program.

Amgen Rat EST Program

Unpublished (2003)

Contact: Dan Fitzpatrick

Amgen, Inc

One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30.6%; Score 30.6; DB 6; Length 461; 36.7%; Pred. No. 16; ive 19; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
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/mol_type="mRNA"
/strain="CZECH II"
/db_xref="taxon:10090"
                                                                                                                                                                                                                                                                                                           Out August 1805 447-4881
Plate: 00015 row: c column: 9.
Location/Qualifiers
Rattus norvegicus (Norway rat)
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Mus musculus
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120 TGAGCAGTTGCATTAGCAA 102
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22 GGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCUU 81
                                                                                                                                                                                                                                                             5', mRNA sequence.
CK016754
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503 TAAGTAGTAG 594
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                                                                            82 AGCG 85
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AUTHORS
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Direct Submission

Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, TT=1:81-45-503-9111, Fax:81-45-503-9170, Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of
                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG069018 917 bp DNA linear GSS 03-NOV-2001
Pan troglodytes DNA, clone: PTB-059H17.R, genomic survey sequence.
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                                                                        /clone lib="NCI_CGAP_Lu29"
/note="Organ: lung; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: Not1; cloned unidirectionally. Primer: Oligo dr.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"
                                                                                                                                                                                                                                                                                                                     19 CGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGC 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pan.
                /tissue type="spontaneous tumor, metastatic to mammary.
Stem cell origin."
/lab_host="DH10B"
                                                                                                                                                                                                                                                             Gaps .
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Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library PTB
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/clone_lib="PTB Chimpanzee Male BAC Library"
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/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="PTB-059H17.R"
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39.1%; Pred. No. 20;
tive 18; Mismatches
/clone="IMAGE:3586661"
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Pan troglodytes
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R.Site 1 : SacI
R.Site 2 : SacI.
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/clone lib="NHI ZGC 10"
/note="Vector: pExpress1; Site_1: Not1; Site_2: EcoRV;

Bulk tissue was collected from a whole adult individual
from the Tuebingen strain. Ist strand cDNA was primed with
a Not I - oligo(dT) primer, double-stranded cDNA was
cloned into the Not I and EcoRV sites of pExpress-1.
Library was size-selected for >1 kb fragments. A
                                                                                                                                                                                                                                                                                                           CKO16754 1inear EST 26-NOV-2003
AGENCOURT_16544280 NIH_ZGC_10 Danio rerio CDNA clone IMAGE:7043617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contract: Daniels 3. Gerhard, Ph.D.
Contract: Daniels 3. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10AO7 Bethsdda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Len Zon, Harvard
CDNA, Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14803 row: i column: 23
High quality sequence stop: 594.
366 GGTATCTGTCGTCCCCCCCCCTCCTACTGGGGTTATAAATGGATTTAAAATTATACCTT 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Actinopterygii, Neopterygii, Teleostei; Ostariophysi, Cyprinidae; Danio.

1 (bases 1 to 725)

11 (bases 1 to 725)

12 (bases 1 to 725)

Nath-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
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/db_xref="taxon:7955"
/clone="IMAGE:7043617"
/tissue_type="whole body"
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/organism="Danio rerio"
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                                                                                                                                                                                                                                                                                                                                                                                                                                       CK016754.1 GI:38541867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Danio rerio (zebrafish)
Danio rerio
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermartophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                       Library was constructed by Corina Guder / GATC Konstanz, Germany Library materials provided by Thomas Holstein / Molecular Cell Biology, TUD, Darmstadt DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Hans Bode (hrbode@uci.edu) Seq primer: 400P High quality sequence stop: 565.
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Singh,J.A., Robert,L.S., Lu,B., Zhu,L., De Moors,A., Couroux,P.,
Harris,L.J., Hattori,J.I., Ouellet,T., Sprott,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Glycine max (soybean)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Singh,J.A.
Eastern Ceral and Oilseed Research Centre
Agriculture and Agri-food Canada
KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KlA
Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, N. Gibbons, M., Ritter, B., Bennett, J., Ronko, I., Tasgarelshvili, R., Maguire, L., Kennedy, S., Waterston, R. and Wilson, R. WashU Hydra EST Project
Whyllished (2002)
Other ESTs: tae26908.x1
Contact: Hans Bode
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 AGGCAUAUGUCGACUCCGUCUUCCAUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCU
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                                                                                                                                                          WashU Hydra EST Project
Washington University School of Medicine
444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db xref="taxon:6085"
/lab_host="TransforMax EC100 (Epicentre), Tl Phage resistant electrocompetent cells"
/clone lib="Hydra EST Darmstadt I"
/note="Wyetcor: pBluescript II SK (+); Site_1: Not1; Site_2: EcoRI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/strain="8f-1 mutant of strain 105"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Hydra magnipapillata"
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BG838990.1 GI:14205312
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393 CAACGAGATCAAGTTT 378
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Glycine max
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Fax: (613) 759-1701
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                                                                                                                                                                                                                                                                                                                                                             Use of a random human BAC End Sequence Database for Sequence-Ready Map Building
L Unpublished (1998)
Other GSSS: CIT-HSP-2374K6.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CN553623 578 bp mRNA linear EST 03-MAY-2004 tae26g08.yl Hydra EST Darmstadt I Hydra magnipapillata cDNA 5' similar to TR:Q9VJZ2 Q9VJZ2 CG6565 PROTEIN. ;, mRNA sequence.
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                                                   GSS 29-AUG-1998
                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
I (bases I to 528)
Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazca; Cnidaria; Hydrozoa; Hydroida; Anthomedusae; Hydridae; Hydra.
Hydridae; Hydra.
Hobses I to 578;
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q., Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cell type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                        CIT-HSP-2374K6.TF CIT-HSP Homo sapiens genomic clone 2374K6
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                                                   linear
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36.9%; Pred. No. 30;
tive 19; Mismatches
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2374K6"
                                                     528 bp
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                                                                                                    genomic survey sequence
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                                                                                                                                        AQ108017.1 GI:3484196
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Hydra magnipapillata
                                                                                                                                                                                       Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /sex="Male
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
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Best Local Similarity
                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                  Venter, J.C.
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                                                     AQ108017
       RESULT 9
AQ108017/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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CN553623/c
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394

EST 25-MAY-2001

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1 (bases 1 to 717)
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Hatiner, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, E., Bennett, J., Ronko, I., Tsagareishvili, R.,
Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
Unpublished (2002)
Contact: Hans Bode
                                                                                                                                                                                                                                                                                                                                                                                           Email: 1916 to the transfer of transfer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hydra magnipapillata
Eukaryota, Metazoa, Cnidaria, Hydrozoa, Hydroida, Anthomedusae,
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                                                                                                                                                                                                                                                                                                                                                     21 AGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCU
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resistant electrocompetent cells"
/clone_lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI;
Site_2: EcoRI"
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone lib="Hydra EST Darmstadt I"
/note="Vector: pBluescript II SK (+); Site_1: NotI; Site_2: EcoRI"
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                                                                                                                                                                                                                                                                                     29; Indels
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/strain="sf-1 mutant of strain 105"
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/lab_host="TransforMax EC100
                                                                                                                                                                                                                     ch 29.6%; Score 29.6; D
I Similarity 40.8%; Pred. No. 36;
31; Conservative 16; Mismatches
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llarity 40.8%; Pred. No. 37;
Conservative 16; Mismatches
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437 CAACAAGATCAAGTTT 452
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Fax: 314 286 1810
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                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 31; Conserv
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nes 31; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                /dev_stage="15-day seedlings"
/clone_lib="Gm01_AAFC_ECORC_Glycine_max_cold_stressed_leav
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Bode, H., Blumberg, B., Steele, R., Wigge, P., Gee, L., Nguyen, Q.,
Martinez, D., Kibler, D., Hampson, S., Clifton, S., Pape, D., Marra, M.,
Hillier, L., Martin, J., Wylie, T., Dante, M., Theising, B., Bowers, Y.,
Gibbons, M., Ritter, B., Bennett, J., Ronko, I., Tasqareishvili, R.,
Maguire, L., Kennedy, S., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: Bluescript SK-/Xhol-EcoRI; Site_1: EcoRI; Site_2: Xhol; Plants were grown 12 days from seeds, treated at 2oC for 3 days, then leaves were collected. Library was prepared using Unizap ZAP-cDNA synthesis kit / Packaged Gigapack III Gold."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydra magnipapillata
Hydra magnipapillata
Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
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/lab_host="TransforMax EC100 (Epicentre), Tl Phage
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4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
TTel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Indels
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/strain="sf-1 mutant of strain 105"
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29.6%; Score 29.6; D
Best Local Similarity 42.4%; Pred. No. 36;
Matches 36; Conservative 14; Mismatches
                                                                                                                                              /mol_type="manh"
cultivar="Maple Arrow"
/db_xref="taxon:3847"
/clone="Gmol_01e04"
/tissue_type="Leaves"
                                                                                                                   organism="Glycine max"
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High quality sequence stop: 626.
Location/Qualifiers
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                                                  Location/Qualifiers
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CN623811.1 GI:47134888
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WashU Hydra EST Project
                       singhja@agr.gc.
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EST analysis of brain and testis cDNA libraries from White leghorn and Red Jungle Fowl

Lundublished (2004)

Lontact: Peter Savolainen
Department of Biotechnology
Royal Institute of Technology, KTH
SE-106 91 Stockholm, SWEDEN
Tel: +46 (0)8 5337 8431
Fax: +46 (0)8 537 8335
Email: Peter Savolainen@biotech.kth.se
Seq primer: M13 reverse primer.

Seq primer: M13 reverse primer.
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                                                                                                                                CN226782 744 bp mRNA linear EST 09-APR-2004 NJE004H01.abl RJtestis Gallus gallus CDNA 5', mRNA sequence.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Silva, C.S., Jorge, E.C., Patricio, M., Ledur, M.C. and Coutinho, L.L.
Discovery of new genes expressed in the chicken pituitary and
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//note="Organ: testis, Vector: pSPORT-1; Site 1: Hind III
Site_2: EcoRl; The cDNA libraries were created with the
Superscript Plasmid System (Invitrogen)."
                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 744)
Savolainen, P., Fitzsimmons, C.J., Arvestad, L., Andersson, L. and
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55.8%; Pred. No. 37;
tive 9; Mismatches
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/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Red junglefowl"
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/sex="male"
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Contact: Clarissa S. Silva
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EARLO - University of Son Paulo

BASLAGO - University of Son Paulo

Fax: 55 19 3429 443

Email: casilva@esalq.usp.br and llcoutin@esalq.usp.br

FRATISES 19 3429 4438

Email: casilva@esalq.usp.br and llcoutin@esalq.usp.br

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BACKWARD: T.

(organism="allus gallus"

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1. /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2. /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

3. /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

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US-09-949-016-1206

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US-09-949-016-12508

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DEFLICANT: GATY L. Breton et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 608
                                                                                                             Sequence 1, Appli
Sequence 1, Appli
Sequence 12, Appl
Sequence 4695, Ap
Sequence 42, Appl
Sequence 42, Appl
Sequence 42, Appl
           Sequence 12838, A
Sequence 17458, A
Sequence 3, Appli
Sequence 15958, A
Sequence 1916, Ap
Sequence 16492, A
Sequence 16494, A
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APPLICANT: Strauss et al.
TITLE OF INVENTION: Floral homeotic genes for manipulation of flowering in TITLE OF INVENTION: Poplar and other plant species.
TITLE OF INVENTION: poplar and other plant species.
FILE REFERENCE: 53375
CURRENT APPLICATION NUMBER: U3/99/410,464
CURRENT FILING DATE: 1999-10-01
EARLIER APPLICATION NUMBER: 09/287,700
EARLIER APPLICATION NUMBER: 60/080,851
EARLIER FILING DATE: 1998-04-06
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin Ver. 2.0
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                      US-09-949-016-17458
US-09-751-389-3
US-09-513-9996-35958
US-09-328-352-1916
US-09-949-016-16492
US-09-949-016-16493
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1 US-09-643-99A8-1

US-09-706-228-12

US-09-248-796A-4695

US-09-295-762-42

US-09-106-582-42

US-09-106-582-42

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US-09-159-469-42
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   :||::: || :|:
TCTGGTTTATGCGTATATTCTAGATTCA 14
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                                                                                                                                                                                                                                                                                                                     Sequence 608, Application US/09328352
Patent No. 6562958
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-410-464-1, Sequence 1, Application US/09410464; Patent No. 6395892
                       57178
786431
246
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47781
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Best Local Similarity
Matches 35; Conserv
US-09-328-352-608/c
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287 ITTTAAAAGTCGCTGAACCAACCGAAGATTCTG 319
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419 SEVENTH STREET, N.W., SUITE 300
                    67 UUUAGCAUAUGCCUUAGCGACAGCAGCUUCUG 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DIAMOND=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/675,773B
FILING DATE: 03-JUL-1996
CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17037, Application US/09949016 Patent No. 6812339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                      Sequence 3, Application US/08675773B Patent No. 6166288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Floppy disk
IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: COOPER, IVER P.
REGISTRATION NUMBER: 28,005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | : | |||
564 CATGGGGACTTGATGCT 548
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  79 CUUAGCGACAGCU 95
                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: DIAMOND, LISA E
APPLICANT: LOGAN, JOHN S
APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic)
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
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US-09-949-016-17037/c
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                                                                                                                  RESULT 5
US-08-675-773B-3/C
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                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 21723
LENGTH: 405
                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster FILE REFERENCE: File Reference: 7326-094

CURRENT APPLICATION NUMBER: US/09/270,767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 27.4%; Score 27.4; DB 4; Length 405; 1 Similarity 35.5%; Pred. No. 2.7; 33; Conservative 19; Mismatches 41; Indels
                                                                                                                32; Indels
                                                                         Query Match
29.8%; Score 29.8; DB 3;
Best Local Similarity 33.3%; Pred. No. 0.77;
Matches 27; Conservative 22; Mismatches 32;
                ORGANISM: Populus balsamifera subsp. trichocarpa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287 ITTTAAAAGTCGCTGAACCAACCGAAGATTCTG 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 UUUAGCAUAUGCCUUAGCGACAGCAAGCUUCUG 99
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; Sequence 21723, Application US/09270767
; Patent No. 6703491
                                                                                                                                                                                                                                                            1253 TTATGATTTTTCTTAGATACA 1273
                                                                                                                                                                                                                                                                                                                                                                        Sequence 6441, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
                                                                                                                                                                                                                                    68 UNAGCAUAUGCCUUAGCGACA 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) ORGANISM: Drosophila melanogaster US-09-270-767-6441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               , ORGANISM: Drosophila melanogaster US-09-270-767-21723
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Best Local Similarity
Matches 33; Conserv
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Best Local Similarity
Matches 33; Conserv
                                                                                                                                                                                                                                                                                                                                 RESULT 3
US-09-270-767-6441
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                    ; ORGANISM: FO
US-09-410-464-1
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TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1307
CURRENT APPLICATION NUMBER: US/09/949,016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 19 CGAGGCAUAUGUCGACUCCGUCUUCCTUCAAACCAGUUAUAAAUUGGUTUUAGCAUAUGC
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APPLICANT: BYRNE, GUERARD W
APPLICANT: SHARMA, AJAY
TITLE OF INVENTION: METHOD OF PRODUCING TRANSGENIC ANIMALS
TITLE OF INVENTION: FOR XENOTRANSPLANTATION.
UNDBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31; Indels
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203 ATTAACACAACTGTCAAGTCTGCCTTTAAAAAACCCAGGTTGACATTTGCTTCATC 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 AUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCAAACCAGUUAUAAAUUGGUUUUAGC 72
APPLICANT: Giordano, J.Y.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
Patent No. 6783961
FILE REPERBYCE: 59.U52.REG
CURRENT FILING DATE: 2000-02-24
PRIOR FILING DATE: 2000-02-26
NUMBER OF SEQ ID NOS: 36681
SEQ ID NO 21500
LENGTH: 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15; Mismatches 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                               27.0%; Score 27; Di 39.8%; Pred. No. 3;
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US-09-513-999C-21500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity 39.8
Matches 33; Conservative
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                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
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LOCATION: 340
OTHER INFORMATION: y=c
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NAME/KEY: misc_feature
LOCATION: 344
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ORGANISM: Homo sapiens
FEATURE:
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SEQ ID NO 26061
LENGTH: 415
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APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REPERENCE: CL001307
CURRENT APPLICATION NUMBER: 60/241,755
PRIOR APPLICATION NUMBER: 60/241,756
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                   Length 260286;
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  CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR PILING DATE: 2000-10-03
PRIOR PILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FASEUSEQ for Windows Version 4.0
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Sequence 21500, Application US/09513999C
Fatent No. 6783961
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Duclert, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-949-016-12106/c
; Sequence 12106, Application US/09949016
; Patent No. 6812339
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Best Local Similarity 39.0%
Matches 30, Conservative
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Best Local Similarity 39.05
Matches 30; Conservative
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ORGANISM: Human
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                                                                                                                                                                                                     SEQ ID NO 17037
LENGTH: 260286
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LENGTH: 260293
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DB 4; Length 208;

Indels

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US-09-513-999C-26061/C

| Sequence 26061, Application US/09513999C
| Sequence 26061, Application US/09513999C
| Patent No. 6783961
| GENERAL INFORMATION:
| APPLICANT: Duclert, A. |
| APPLICANT: Glordano, J.Y. |
| TILLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins. |
| Patent No. 6783961 |
| FILE REFERENCE: 59.US2.REG |
| CURRENT APPLICATION NUMBER: US/09/513,999C |
| CURRENT FILING DATE: 1209-02-24 |
| PRIOR APPLICATION NUMBER: US 60/122,487 |
| PRIOR APPLICATION NUMBER: US 60/122,487 |
| PRIOR PILING DATE: 1999-02-26 |
| COMMISSIONED OF TABLET OF TA
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10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 26.8%; Score 26.8;
Best Local Similarity 48.4%; Pred. No. 4.
Matches 30; Conservative 10; Mismatche
                                                                                                143 ATATTCAGACCCCCAGCTAGCT 121
73 AUAUGCCUUAGCGACAGCU 95
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94639 AGGAAGGCTTTGATGCACAATTTCTCTCCAAAATCCATTCAAGTACCAAAAAGTTCTTCC. 94580
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CITY: Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 162, Application US/08956171E
Patent No. 6593114
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20850
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; LOCATION: (1)...(150597)
; OTHER INFORMATION: n = A.
US-09-949-016-15379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc feature LOCATION: (1)...(15059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                   US-09-949-016-15379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-956-171E-162
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                                                                                                                         Sequence 3637, Application US/09949016

Sequence 3637, Application US/09949016

Patent No. 681239

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT PILING DATE: 2000-04-14

PRIOR FILING DATE: 2000-10-20

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PRILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FRACEOF FOR WINDOWS VETSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1753, Application US/09949016

Sequence 1753, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR PELING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/231,768

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PILING DATE: 2000-10-03

PRIOR FILING DATE: 2000-10-03

WINMER OF SEQ ID NOS: 207012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 26; DB 4; Length 6944;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9; Mismatches
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Best Local Similarity 38.9%;
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Matches 38; Conservative
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                AG 208
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ORGANISM: Human
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US-09-949-016-17553
                                                                                                               US-09-949-016-3637
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LENGTH: 6944
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Sequence 15379, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
TITLE OF INVENTION WIMBER: US/09/949,016

CURRENT APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR PLING DATE: 2000-10-03

PRIOR PELING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FESTESQ for Windows Version 4.0

SEQ ID NO 15379

LENGTH: 150597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fannon
TITLE OF INVENTION: Staphylococcus aureus Polymucleotides and Sequences
NUMBER OF SEQUENCES: 5256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10 GGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26.0%; Score 26; DB 4; Length 150597; 46.3%; Pred. No. 64; Live 9; Mismatches 35; Indels 0.
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OPERATING SYSTEM: MSDOS version 6.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc
                                    69 UAGCAUAUGCCUUAGCGACAGCAUCU 98
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                           linear
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ORGANISM: Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-949-016-12508
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                                                                                                           ; TOPOLOGY: ]
US-08-781-986A-162
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22 GGCAUAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCUU 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25.8%; Score 25.8; DB 4; Length 798; 31.2%; Pred. No. 13; tive 21; Mismatches 32; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                                APPLICATION NUMBER: US/08/956,171E
                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/009,861
FILING DATE: January 5, 1996
APPLICATION NUMBER: 08/781,986
FILING DATE: January 3, 1997
ATTORNEY/AGENT INPORMATION:
REGISTRATION NUMBER: 46,789
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8439
INFORMATION FOR SEQ ID NO: 162:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear SEQUENCE DESCRIPTION: SEQ ID NO: 162: US-08-956-171E-162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/08/781,986A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 162, Application US/08781986A Patent No. 6737248
                                                                 FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB246
TELECOMMUNICATION INFORMATION:
TELECHONE: (301) 309-8504
TELEFAX: (301) 309-8512
                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 798 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         256 CGCTTCTGCGATTTTCT 272
                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 AGCGACAGCAAGCUUCU 98
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Best Local Similarity 31.24
Matches 24; Conservative
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
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US-08-781-986A-162
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SEQUENCE CREATERISTICS:

SEGURATE CREATERISTICS:

TYPE: Incleic acid
STRANDEDERSS:

STRANDEDERSS:

STRANDEDERSS:

Outery Match
STRANDEDERSS:

STRANDEDERSS:

Outery Match
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RESULT 1
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AC125279 MUS MUSCU
AC110847 Rattus no
AC110697 Rattus no
AC110697 Rattus no
AC129051 Rattus no
AC129051 Rattus no
AC129051 Rattus no
AC23051733 Sequence
CQ3637795 Sequence
CQ3637795 Sequence
AF522912 Tachyglos
AF522912 Tachyglos
AF522916 Tachyglos
AF522916 Tachyglos
AC137177 Rattus no
AC137177 Rattus no
AC137177 Rattus no
                                                                      April 19, 2005, 13:28:09; Search time 1693 Seconds (without alignments) 2862.092 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
                                                                                                                                                                                                              4708233 segs, 24227607955 residues
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Maximum Match 100%
Listing first 45 summaries
                                                OM nucleic - nucleic search, using sw model
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AC125279
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AF522912 AF522914
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AC137289
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AR318058
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AC099144
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length DB
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gb htg: *
gb om: *
gb ow: *
gb ph: *
gb ph: *
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gb_nn:
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Perfect score:
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AC131482 Rattus no	AC139588 Rattus no	AC110146 Rattus no	AC112576 Rattus no	CR536601 Platypus	AC109911 Rattus no	AC131223 Rattus no	AC095368 Rattus no	AC133102 Mus muscu	AR372457 Sequence	AF057708 Populus b	AC103805 Homo sapi	AC145887 Pan trogl	AC067941 Homo sapi	CR450730 Danio rer	AC148836 Pan trogl	AC018216 Drosophil	AC117541 Mus muscu	AC002443 Drosophil	Continuation (4 of	Continuation (5 of	AC093047 Drosophil	AC145913 Gallus ga	AC093440 Drosophil	AC106118 Rattus no	AC137343 Rattus no	
AC131482	AC139588	AC110146	AC112576	CR536601	AC109911	AC131223	AC095368	AC133102	AR372457	AF057708	AC103805	AC145887	AC067941	CR450730	AC148836	AC018216 ·	AC117541	AC002443	AC110832 3	AC112373 04	AC093047	AC145913	AC093440	AC106118	AC137343	
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## ALIGNMENTS

AC084053	
cocus	AC084053 199415 bp DNA linear ROD 05-SEP-2002
OEFINITION	Mus Musculus Strain C5/BL6/J chromosome 3 BAC, KF23-158F1, Complete semience.
ACCESSION	
/ERSION	AC084053.6 GI:22725947
CEYWORDS	
SOURCE	Mus musculus (house mouse)
ORGANISM	
	Mammalia: Butheria; Kodentia; Sciurognatni; Muridae; Murinae; Mus.
ATTHORS	I (bases I to 199415) Han J. Montdomerv K.T. Grilla.G. Chiu.D. Decker.J. Fusina.M.
	Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,
	Perera, A., Shim, C., Thomas, E. and Kucherlapati, R.
TITLE	High Throughput Mouse Sequencing
JOURNAL	Unpublished
REFERENCE	2 (bases 1 to 199415)
AUTHORS	Han, J., Montgomery, K.T., Grills, G., Chiu, D., Decker, J., Fusina, M.,
	<pre>Goltz,J., Haider,A., Hall,L., Ioshikhes,I.P., Lee,E., Long,J.,</pre>
	Perera, A., Shim, C., Thomas, E. and Kucherlapati, R.
TITLE	Direct Submission
JOURNAL	Submitted (12-OCT-2000) Department of Molecular Genetics, Albert
	Einstein College of Medicine Genome Center, 1300 Morris Park Ave.,
	Bronx, NY 10461, USA
REFERENCE	3 (bases 1 to 199415)
AUTHORS	Han, J., Montgomery, K.T., Grills, G., Chiu, D., Decker, J., Fusina, M.,
	Goltz, J., Haider, A., Hall, L., Ioshikhes, I.P., Lee, E., Long, J.,
	Perera, A., Snim, C., Thomas, E. and Kucherlapaci, K.
TITLE	
JOURNAL	
	Genomics, Harvard Medical School, 65 Landsdowne St, Cambridge, MA 02139. USA
REFERENCE	4 (bases to 199415)
AUTHORS	Han, J., Montgomery, K.T., Grills, G., Chiu, D., Decker, J., Fusina, M.,
	Derera A. Shim.C. Thomas E. and Kucherlabati.R.
TITLE	Direct Submission
JOURNAL	Submitted (05-SEP-2002) Harvard Partners Center for Genetics and Genemics Harvard Medical School 65 Landedowns St. Cambridge MA

family="L1MA7"

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STSs are identified using ePCR (Genome Res. 7:541-550).
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences (A. Smit and P. Green, Genes and Regions of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to EST and cDNA sequences in Unigene. Genes demonstrate at least two exons flanked by consensus splice sites that maintain sequence continuity matches are annotated as similar.
                                                                                                                                                                                                                         CLONE LENGTH: This sequence represents the entire insert of this clone unless otherwise noted. If there are overlapping clones, the overlaps are noted in the beginning and end of the Features
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCING READ COVERAGE: Attempts are made to complete double strandedsequence for all regions. All sequence is completed to a standard of coverage with a minimum of 3 reads with no ambiguities. If the sequence coverage for a region does not meet this standard, it is indicated in the amnotation aslow Coverage. Low coverage linkages are verified by PCR product size verification or verification of forward and reverse reads from clones which span
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated average error rate is less than 1 per 10,000 bases using the Consed quality parameters. Regions that do not meet this requirement are annotated as Low Quality.
Sep 5, 2002 this sequence version replaced gi:22002115.
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                                                                                         Center Code: HPGC
Web site: http://www.hpcgg.org/Sequence/mouse.html
Contact: hpgc@mendel.mgh.harvard.edu
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Contig length: 199415
Fraction of Phrap value < 40: 0.000326
Error Rate in Consed: 0.00 per 10,000 bases
Number of N's in consense: 0
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Phrap Value Range
                                                              Harvard Partners Genome Center
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Chemistry: Dye-terminator Big Dye; 100$
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Center project name: ADW
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complement(557. .1289)
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COMMENT
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/ryt family="CT-rich"
complement (15461. 15814)
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complement (15461. 15814)
/rpt family="MJT2B3"
complement (15831. 15915)
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complement(7008. .7281)
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complement'
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complement(11152, 11712)
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064. 9076
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complement(1392. .1889)
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                                                complement (1888. .3694)
                                                                                                                                               complement(5123..5507)
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complement(5512..6982)
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                                                                                              252. .444i
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796. .9882
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.17159
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                                                             rpt_family="Lx"
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Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see
                                                                                                                                                                                      The RPCI-23 BAC Library has been constructed by Kazutoyo Osegawa and Minako Tateno in the laboratory of Pieter de Jong (http://www.chori.org) from female C57BL/61 mouse kidney and/or brain genomic DNA. The clone and detailed information can be obtained from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at http://www.chori.org
                                                                                                                                                                                                                                                                                                                                                             This sequence is the entire insert of the clone. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             NEIGHBORING SEQUENCE INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
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/chromosome="8"
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171. .557
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5516. .5712 - "MALR"
/rpt_family="MaLR"
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rpt_family="L1"
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0485. .10610
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1792. .2918
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                                                                                                                               http://genome.wustl.edu
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2674. .12714
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                                           MAPPING INFORMATION:
                                                                                                                                                                      SOURCE INFORMATION:
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Submitted (05-NOV-2003) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ROD 05-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (21-JUN-2002) Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO 63108, USA (bases 1 to 201197)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1 (base 1 to 20197)

Trani,L. and Cotton,M.

The sequence of Mus musculus BAC clone RP23-433F5
                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                   AC125279 201197 bp DNA linear ROD 05-N
Mus musculus BAC clone RP23-433F5 from 8, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                           37 CGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUAGCAUAUGCCUUAGCGACAG 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Center: Washington University Genome Sequencing Center
Center code: WUGSC
                                                                                                                                                                                                                                                                                                                     Length 199415;
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                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                 13;
                                                                                                                                                                                                                                                                                                                       DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                     ; Score 32.2; DE; Pred. No. 8.6; 14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: M_BA0433F05
                                                                                                                                                                                        /rpt_family="\underser".complement(25288. .25661)
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25183, .25208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing of Mus musculus Unpublished (2001) 3 (bases 1 to 201197) McPherson, J. D. and Waterston, R.H.
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family="(GAAA)n"
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                                                                                                                                                                                                                                                                                                                                                               26; Conservative
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25210.
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RESULT 2 AC125279/c LOCUS

Matches

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DEFINITION

ACCESSION VERSION

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JOURNAL REFERENCE AUTHORS

AUTHORS REFERENCE

TITLE

TITLE JOURNAL REFERENCE AUTHORS

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AUTHORS JOURNAL

COMMENT

REFERENCE

Length 201197;

Indels

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Rattus.

Rattus.

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Rattus.

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Rattus.

Ruzny, D. Marie. . Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebech, V., Aoyagi, A., Ayodeji, M., Baca, B., Badan, H.,

Baldwin, D., Bandaranatke, D., Barber, M., Barnstead, M., Benahmed, F.,

Baldwin, D., Bandaranatke, D., Burrell, K., Calderon, E.,

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Davila, M.L., Davis, C., Durn, A., Pubrin, K., Duval, B., Eaves, K.,

Egan, A., Becotto, M., Elagg, N., Forbes, L., Foster, M., Gebregeorgis, E., Geer, K., Gill, K., Grady, M., Garera, W., Gebregeorgis, E., Geer, K., Gill, K., Grady, M., Garera, W., Gebregeorgis, E., Geer, K., Gill, K., Grady, M., Hendarson, N., Hernandez, M.,

Harvey, X., Havlah, W., Hamil, C., Hamilton, K., Hogues, M.,

Harvey, X., Haulah, W., Hamil, C., Hamilton, K., Johnson, R., Mandum, M., Mandum, J., Liu, W., Liu, Y., Man, J., Liu, Y., Man, J., K., Martin, K., Martin, R., Martin, S., Pul, L.-L.,

Plopper, P., Polindexter, A., Polor, C., Plopper, P., Polindexter, M., Poer, R., Polindexter, P., Polindexter, P., Polindexter, P., Polindexter, R., Pol
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rattus norvegicus clone CH230-42M10, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                     2984 GCAGGCTTTCATCCCAGCATCTGATTCCTGAGTCTTCATTGATAAATCTAACAATTGAG 2925
                                                                                                                                                                                                                                            7 GGAGGAAUUCAUCGAGGCAUAUGUCGACUCCGUCUUCCAUCAAACCAGUUAUAAAUUGGU 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                               DB 10;
                                                                                                                                                                                                                                                                                                                                                     67 UUUAGCAUAUGCCUUAGCGACAGCUUCU 98
                                                                                                                                                             31.2%; Score 31.2; D
32.6%; Pred. No. 19;
ive 24; Mismatches
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Matches 30; Conservative
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:=-11.21)"
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2775. .22988
rpt_family="MER1_type"
2991. .23088
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7. .33276
family="Alu"
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6324. 346.1
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omplement(26924.
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8352. .18653
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1030. .21117
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6795. .36891
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881<u>8</u>.
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6145.
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4784.
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5040
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6862.
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0593.
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us-09-529-397c-25.rge

AUTHORS TITLE JOURNAL

TITLE JOURNAL REFERENCE REFERENCE AUTHORS TITLE JOURNAL

COMMENT

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ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission

L. Submitted (15-7002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

ON NOW 15, 2002 this sequence version replaced gi:23321762.

The sequence in this assembly is a combination of BAC based reads and whole genome shorpun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each coning described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the serimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NOTE: Batimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html). NOTE: This is a 'working draft' sequence. It currently consists of 13 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Steed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,B., Thomas,B., Thomas,B., Used,B., Waldron,L., Walker,B., Usmanl,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Warnen,R., Wei,X., White,F., Willson,R., Willeon,R., Willeon,R., Willeon,R., Willeon,R., Willeon,R., Willeon,R., Willeon,B., Yon,J., Yakub,S., Yen,J., Yoon,L., Yoon,V., Will,F., Zhou,J., Zhou,X., Zhao,S., Dunn,D., Yon Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O., Weinstock,G. and Gibbs,R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31167: contig of 31167 bp in length 31267: gap of unknown length 77383: contig of 46116 bp in length 77483: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contig of 91428 bp in length
gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            169011: gap of unknown length
170421: contig of 1410 bp in length
170521: gap of unknown length
172029: contig of 1508 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center: Baylor College of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 187606)
Rat Genome Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 187606)
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                                                                                                                                                                                                                                                                                                                                                         Direct Submission
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Worley, K.C.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31168
31268
77384
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169012
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170522
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AC103165 221981 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-194N19, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HTG; HTGS PHASE2; HTGS DRAFT; HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
Rattus norvegicus (Sorway rat)
Bukaryota; Metazoa; Chordara; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 187606;
                                                                                                                                                           יה קי
length
יי length
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                                  length
bp in length
                                                                   length
bp in length
                                                                                                                                                                                                                                                            in length
                                                                                                                      contig of 2122 bp in length
                                                                                                                                                     bp in length
                                                                                                                                                                                                                           in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  62 UNGGUUUUAGCAUAUGCCUUAGCGACAGCAAGCUUCUG 99
                                                                                                                                                                                                                                           length
Length
                                                                                                      ength
                                                                                                                                         ength
                                                                                                                                                                                                            length
                                                                                                                                                                                                                                                                                                                 /organism="Rattus norvegicus"
                                                                                                                                                       contig of 1342
gap of unknown
                                                                                                                                                                                                                                           184591: gap of unknown
187606: contig of 3015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.8%; Score 30.8; D
34.7%; Pred. No. 26;
ive 22; Mismatches
                                                                                                        unknown
                                                                                                                                                                                        182073: contig of 1543
182173: gap of unknown
                                                                                                                                                                                                                           184491: contig of 2318
                                  unknown
                                                     of 1297
                                                                     unknown
                                                                                    of 1562
                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                 /mol_type="genomic DNA
/db xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                      /clone="CH230-42M10"
                                                 contig
gap of contig
                                                                                                                                                                                                                                                                                Location/Qualifiers
                  contig
gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="wgs_contig"
95087. .96968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="wgs_contig"
45131. .150091
                                                                                                                                          gap of
                                                                                                                                                                                                                                                                                                                                                                                                       /note="wgs_contig"
28318. .29829
                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="wgs_contig"
77484. .79244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="wgs_contig"
131603. .132754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    note="wgs_contig"
67411. .168911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note="wgs_contig"
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                                                                                                                                                                                                                                                                                                                                                                                        .15402
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                                                                                                                        .78988:
                                                                                                                                          .79088:
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Best Local Similarity 34.7%
                                                                                                                                                                                                                                                                                                                                                                                        13985
                                                                                                                                                                                                                                           184492
                                    73708
73808
                                                                   175105
                                                                                                                                                         79089
                                                                                                                      176867
                                                                                                                                          78989
                                                                                                                                                                                                                             82174
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KEYWORDS
SOURCE
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Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Dinny, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Durna, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eduge, C., Evans, C.A., Falls, T., Falls, T., Falls, M., Plages, K., Garcia, A., Garrar, M., Gabrisi, A., Ganta, R., Garcia, A., Garrar, M., Gabrisi, A., Ganta, R., Garcia, A., Garrar, M., Guerra, M., Gubergeorgis, E., Gaer, K., Gill, R., Garcia, A., Garrar, M., Guerra, M., Gubergeorgis, E., Haaland, M., Hamil, C., Hamilton, C., Hamilton, K., Harnandez, R., Hines, S., Hlayk, B., Hume, J., Idlebird, D., Jackson, A., Hollins, B., Howells, S., Hlayk, S., Hume, J., Idlebird, D., Jackson, A., Karpath, S., Kelly, S., Kolly, S., Kelly, M., Martinez, B., Mandiar, M., Martinez, B., Mandiar, M., Martinez, B., Mandiar, M., Martinez, B., Mandenhor, O., Okwonu, G., Olarnpunasyor, J., Pera, J., Ferank, S., Pere, J., Rear, M., Rose, R., Rus, S., Pelly, M., Savery, G., Scherer, S., Soretle, R., Reigh, R., Kelly, M., Savery, G., Scherer, S., Soretle, R., Warg, C., Usmail, K., Warten, R., Ware, M., Norle, S., Warten, R., Warten, R., Warten, R., Warten, R., Warten, R., Warten, S., Wart
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The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas and whole genome shotgun sequencing reads assembled using Atlas in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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JOURNAL
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TITLE
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REFERENCE

REFERENCE

JOURNAL

COMMENT

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AC114165 231814 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-165814, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                           Muzny, D.Marie., Metzker, M. Lee., Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Angalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Bardaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Carrer, K., Cavaeron, E., Cardenas, V., Carter, K., Cavaes, H., Center, A., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,
                                             Assembly program: Atlas 3.0;
Consensus quality: 210155 bases at least Q40
Consensus quality: 214132 bases at least Q30
Consensus quality: 114132 bases at least Q30
Estimated insert size: 222472; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota; Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 UAUGUCGACUCCGUCUUCCUUCAAACCAGUUAUAAAUUGGUUUUJAGCAUAUGCCUUAGCG
                                                                                                                                                                                                                                                                                          are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 21981: contig of 221981 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2; Length 221981;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HTG; HTGS PHASE2; HTGS DRAFT; HTGS ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Center clone name: CH230-194N19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .1454
/note="wgs end_extension
clone_end:Sp6"
39959_ .40695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30.8%; Score 30.8; 37.8%; Pred. No. 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="genomic DNA"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            end_sequence:BH339559"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39959. .40695
/note="clone_boundary
clone_end:Sp6
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AC114165.4 GI:30579575
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Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davis, C., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Degado, O., Denson, S., Deramo, C., Ding, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, H., Divya, K., Degado, O., Denson, S., Deramo, C., Ding, H., Divya, K., Degado, C., Espain, P., Fan, G., Farnandez, S., Finley, M., Flagg, N., Forbes, L., Poster, M., Foster, P., Francer, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, M., Foster, P., Francer, C.M., Gabisi, A., Galara, R., Garcia, A., Garner, M., Geverra, M., Gebregocrgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, M., Gunarance, P., Hane, S., Hladun, S.L., Hodgson, A., Hogues, M., Herrandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Hladun, S.L., Hume, J., Idlebird, D., Jackson, J., Jang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kally, S., Khan, Z., King, L., Kovar, C., Kraft, C.L., Lebow, H., Levan, J., Lauds, L., Li, Z., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Mangum, A., Mangum, B., Mapue, P., Martin, R., Willber, R., Sadergren, B., Sadergren, B., Stott, G., Shateman, S., Varin, R., Varight, D., Wright, R., Walse, R., Walse, R.
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Baylor plaza, Housenon, TX 77030, USA.

The sequence in this assembly is a combination of BAC based reads and whole genome shortgun sequencin reads assembled using ALIas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence
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Genome Sequencing Consortium.
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AUTHORS
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Center code: BCM Web site: http://www.hgsc.bcm.tmc.edu/

COMMENT

Contact: hgsc-help@bcm.tmc.edu

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230424 GTÁGAGCAGAÁTATCÁTTAGGAGTTÁTTTAATCACTGTTTTTTTTTAÁAGTCATTÁTTÁT 230365
                                                                                                                                                                                                                                              NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a "working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 231814: contig of 231814 bp in length.
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Rattus norvegicus clone CH230-43H7, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC110697
AC110697 GI:25188485
HTG: HTGS_PHASE2; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Assembly program: Atlas 3.0;
Consensus quality: 219004 bases at least Q40
Consensus quality: 222024 bases at least Q30
Consensus quality: 224099 bases at least Q20
Estimated insert size: 229718; sum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
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34.7%; Pred. No. 26;
ive 22; Mismatches
                                               Center clone name: CH230-165B14
Center project Information
                                                                     --- Summary Statistics
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clone_end:T7"
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/db_xref="taxon:10116"
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93963. .96094
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228398. .231814
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clone_end:Sp6
site:EcoR1
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119152. .121641
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Anyalabechi, V., Anyadi, A., Anyadei, M., Baca, E., Baden, H., Baladranale, P., Anyadi, A., Anyadiano, D., Anyalabechi, V., Anyadi, A., Anyadiano, D., Anyalabechi, V., Anyadi, A., Anyadiano, D., Anyalabechi, V., Balatri, J., Barberoke, S., Bilth, P., Barnete, M., Benahmed, F., Biswalo, K., Blatt, J., Blankenburg, K., Blyth, P., Brown, M., Brayal, C., Carter, M., Carer, D., Chen, G., Corle, D., Denemo, C., Corle, D., Diano, J., Carer, C., Corle, D., Diano, J., Carer, C., Corle, D., Diano, J., Chare, D., Chen, G., Corle, D., Diano, J., Davil, M., Cree, D., Donano, S., Daramo, C., Ding, Y., Chan, T., Fan, C., Persper, M., Decaper, M., Dayad, B., Barnete, M., Dayad, C., Corle, D., Danon, S., Daramo, C., Ding, Y., Dinh, H., Daya, K., Dayaga, A., Escotto, M., Elagg, M., Carer, M., Carrer, M., Garrer, M., Hernandez, S., Findun, S.L., Henderson, N., Hernandez, J., Hernandez, M., Havak, P., Havak, P., Hander, M., Handle, D., Danson, M., Havak, M., Hawes, A., Hander, M., Mandlow, R., Martin, K., Martin,
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Baylor Plaza, Houston, TX 77030, USA.

The Sequence in this sequence version replaced gi:23267238.

The Sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated
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Rat Genome Sequencing Consortium.
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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Direct Submission
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AUTHORS TITLE JOURNAL TITLE JOURNAL

COMMENT

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(see http://www.hggc.bcm.tumc.edu/docs/Genbank_draft_data.html).
NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.
This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature
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------- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 212738 bases at least Q40
Consensus quality: 215401 bases at least Q30
Consensus quality: 217067 bases at least Q20
Estimated insert size: 219523; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NOTE: Estimated insert size may differ from sequence length
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                                                                                                                                                                                          Center: Baylor College of Medicine Center code: BCM
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/note="wgs end_extension
clone_end:"]"
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clone_end:T7"
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/db_xref="taxon:10116"
/clone="CH230-43H7"
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85851. .88514
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/note="clone_boundary
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clone_end:Sp6
site:EcoRI
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complement[232161.
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site:EcoRI
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Center project name: GGYP
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site:EcoRI
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                                                                                                                                                                                                                                                                                                                                                     Natary, D. Marie., Metzker, M. Lee., Abramaton, S., Addme, C., Alder, J., Allen, L., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Allen, H., Alsbrooke, S., Amin, A., Anguiano, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Banahmed, F., Bisadon, M., Bendarenak, P., Bruwn, M., Bisadon, K., Buyth, P., Bruwn, M., Braden, D., Career, K., Cavazo, T., Ceasar, H., Cenner, A., Usuval, C., Cavalo, C., Coyle, M., Cree, M., D'Souza, L., Davila, M., Cree, M., Drang, C., Coyle, M., Cree, M., D'Souza, L., Davila, M., Cree, M., Drang, C., Ding, Y., Chin, T., Pan, C., Coyle, M., Cree, M., Drang, C., Daramo, C., Ding, Y., Chin, M., Cree, M., Caree, M., Chen, S., Durn, A., Duthin, K., Duval, B., Eaves, K., Brang, A., Escotto, M., Eugene, C., Ding, Y., Caree, C., Ding, Y., Caree, M., Caree, M., Caree, M., Garee, M., Garee, M., Gareer, M., Gabis, A., Gare, M., Garee, M., Garee, M., Gare, M., Hernandez, S., Fluyk, S., Hulyk, S., Hander, M., Havalk, P., Haves, A., Hulyk, S., Hung, M., Hodgeon, M., Hodgeon, M., Howelle, S., Hulyk, S., Kally, S., Munden, M., Marjum, M., Morris, K., Morris, S., Munden, B., Morris, S., Morris, S., Munden, M., Morris, S., Munden, M., Morris, S., Munden, M., Morris, S., Munden, M., Marjum, M., Morris, S., Munden, M., Morris, S., Barth, M., Marron, R., Warten, R., Warten, R., Warten, R., Warten, M., Warten, S., Warten, S., Warten, S., Warten, S., Warten, S., Warte
                                                        AC099144 238172 bp DNA linear HTG 10-MAY-2003
Rattus norvegicus clone CH230-68F7, WORKING DRAFT SEQUENCE.
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                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                   HTG; HTGS PHASE2; HTGS DRAFT; HTGS FULLTOP
Rattus norvegicus (Norway rat)
Rattus norvegicus
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RESULT 7
AC099144/c
                                                     LOCUS
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Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA on May 10, 2003 this sequence version replaced gi:23264509. The sequence in this sequence version replaced gi:23264509. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequenting reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank draft_data.html).

* NOTE: This is a 'working draft' sequence. It currently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Estimated insert size: 230633; sum-of-contigs estimation Quality coverage: 7x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               shotgun sequence only contigs will be indicated in the feature table.
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This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.

1 238172: contig of 238172 bp in length.
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al Similarity 43.1%; Score 30.8; DB 2; Length 238172;
al Similarity 43.1%; Pred. No. 26;
25; Conservative 16; Mismatches 17; Indels 0:
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Consensus quality: 220106 bases at least Q40
Consensus quality: 222963 bases at least Q30
Consensus quality: 224727 bases at least Q20
Estimated insert size: 230633; sum-of-contigs
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Center code: BCM
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/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-68F7"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hggc-help@bcm.tmc.edu
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clone_end:Sp6"
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clone_end:T7"
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234541. .234906
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/note="clone_boundary
clone_end:T7
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/note="clone_boundary
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/note="wgs_contig"
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Rallen, C. Allen, H. Albabrooks, S. Amin, A. Angulano, D. Allen, C. Allen, H. Albabrooks, S. Amin, A. Angulano, D. Allen, C. Allen, H. Albabrooks, S. Amin, A. Angulano, D. Anyalebechi, V. Avoyaji, A. Ayodeji, M., Baca, E., Baden, H. Balden, V. Buyal, D. Bandaranaike, D. Barber, M. Bars, Baden, H. Balden, E. Baden, M. Balden, D. Bandaranaike, D. Barber, M. Bars, D. Banden, E. Carasol, C. Buyal, C. Buyal, C. Buyal, C. Buyal, C. Buyal, C. Care, D. Care, C. Coyle, D. Danson, S. Daramo, C. Ding, Y. Chin, T. Duyal, B. Eaves, W. Daraper, H. Duyan-Rocha, S. Dum, A. Durbin, K. Duval, B. Eaves, K. Brand, C. Danson, S. Dum, A. Durbin, K. Duval, B. Eaves, K. Brand, C. Care, C. Coyle, M. Carer, M. Carer, M. Gabrager, B. Geer, K. Gilly, M. Guerra, M. Carer, M. Garbar, M. Garran, M. Hernandez, S. Filly, M. Hawes, A. Hander, D. Hamilton, C. Hamilton, C. Handlen, M. Johnson, B. 
129774 GCATATTTCGATTCCTTCTTGCCTTAAACCAATTTGAACGTGGTCTTACAAAATCTCT 129717
                                                                                                                                                                                  AC129051 250740 bp DNA linear HTG 20-NOV-2002
Rattus norvegicus clone CH230-89P7, *** SEQUENCING IN PROGRESS ***,
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                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae,
                                                                                                                                                                                                                                                                                                 AC129051.3 GI:25139158
HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
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Direct Submission
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KEYWORDS
                                                                                                                     RESULT 8
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Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 250740)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (20-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 20, 2002 this sequence version replaced gi:23683080.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.ed/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold') Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence contigs within a contig-scaffold that consist entirely of whole senome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads.
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* (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

* NOTE: This is a "working draft' sequence. It currently

* Consists of 3 contigs. The true order of the pieces

* is not known and their order in this sequence record is

* arbitrary. Gaps between the contigs are represented as

* runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence

* as soon as it is available and the accession number will

* be preserved.
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Assembly program: Prap; version 0.990329
Consensus quality: 217247 bases at least Q40
Consensus quality: 222917 bases at least Q30
Consensus quality: 226268 bases at least Q30
Estimated insert size: 225713; aum-of-contigs estimation
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation
Molecular and Human Genetics, Baylor College of Medicine, One /lor Plaza, Houston, TX 77030, USA
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247785 249178: contig of 1294 bp in length
247875 249178: contig of 1294 bp in length
249279 250740: contig of 1462 bp in length
249279 250740: contig of 1462 bp in length.
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Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
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clone="CH230-89P7"
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/note="wgs_contig"
39370. .40<u>8</u>12
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152186. .153864
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164963. .166515
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Query Match
Best Local Similarity 46.8%
Matches 36; Conservative
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AE017283 06
AE017283 07
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AE017283 15
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                             Gaps
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Propionibacterineae, Propionibacteriaceae; Propionibacterium.
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                                                               DB 2; Length 250740;
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Human polynucleotides and polypeptides encoded thereby
Patent: WO 019523-A 17493 06-DEC-2001;
Curagen Corporation (US)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 748;
                                                             30.8%; Score 30.8; DB 2; Length 2 43.1%; Pred. No. 27; Live 16; Mismatches 17; Indels
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| forganism="Propionibacterium acnes"
| /mol type="unassigned DNA"
| /db_xref="taxon:1747"
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Sequence 17493 from Patent WO0192523.
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46.8%; Pred. No. 20;
vative 12; Mismatches
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CORIXA CORPORATION (US)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .748
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Sequence 78 from Patent WO0181581.
CQ363795.1 GI:41300489
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179234. 181122
/note="wgs_contig"
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Propionibacterium acnes
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CQ451733.1 GI:41420097
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CQ363795
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AE017283_24 240001 2510000
AE017283_25 2500001 2560265
Continuation (16 of 26) of AE017283 from base 1500001 (AE017283 Propionibacterium acnes P
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Tachyglossus aculeatus clone TaG7 type I interferon gene, partial
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Tachyglossus aculeatus
Eukaryota, Metzacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Monotremata; Tachyglossidae; Tachyglossus.
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0
Length 15776;
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                                    29;
30.6%; Score 30.6; DB 6;
46.8%; Pred. No. 25;
tive 12; Mismatches 29;
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AF522912.1 GI:27451581
                                                                                                                                                                                                                                                                                 Sequence split into 26 fragments
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1 (bases 1 to 217)
Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Tachyglossus aculeatus clone TaG31 type I interferon gene, partial
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A survey of type I interferons from a marsupial and monotreme
implications for the evolution of the type I interferon gene i
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                                   A survey of type I interferons from a marsupial and monotreme: implications for the evolution of the type I interferon gene family
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Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Harrison, G.A., Young, L.J., Watson, C.M., Miska, K.B., Miller, R.D. and
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Tachyglossus aculeatus clone TaG11 type I interferon gene, partial
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Monotremata, Tachyglossidae, Tachyglossus.
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Submitted (19-JUN-2002) School of Science, Food and Horticulture,
University of Western Sydney, Locked Bag 1797, Penrith South DC,
NSW 1797, Australia
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Matches 30; Conservative 16; Mismatches 26; Indels
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/organism="Tachyglossus aculeatus"
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1 (bases 1 to 366)
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Breton, G. and Bush, D.
Nucleic acid and amino acid sequences relating to Acinetobacter baumanni for diagnostics and therapeutics
Patent: US 6562958-A 608 13-MAY-2003;
Location/Qualifiers
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                        Query Match 30.4%; Score 30.4; DB 4; Length 217; Best Local Similarity 41.7%; Pred. No. 21; Matches 30; Conservative 16; Mismatches 26; Indels (
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